



## SEQUENCE LISTING

<110> Aharoni, Asaph  
Lucker, Joost  
Verhoeven, Harrie A.  
van Tunen, Arjen J.  
O'Connell, Ann P.

<120> Fruit Flavour Related Genes And Use Thereof

<130> 160721

<140> pct/nl99/00737

<141> 1999-12-02

<150> EP 98204018.0

<151> 1998-12-02

<150> EP 99200739.3

<151> 1999-03-12

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<170> PatentIn Ver. 2.1

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Thr Ile Lys Pro Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu

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acc ctc ctg gac cag ctc act cct ccg gcg tat gtc ccc atc gtg ttc 147			
Thr Leu Leu Asp Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe			
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ttc tac ccc att act gac cat gac ttc aat ctt cct caa acc cta gct 195			
Phe Tyr Pro Ile Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala			
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gac tta aga caa gcc ctt tcg gag act ctc act ttg tac tat cca ctc 243			
Asp Leu Arg Gln Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu			
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tct gga agg gtc aaa aac aac cta tac atc gat gat ttt gaa gaa ggt 291			
Ser Gly Arg Val Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly			
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Val Pro Tyr Leu Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu			
95	100	105	
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Arg Leu Arg Lys Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro			
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Phe Ser Met Glu Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val			
125	130	135	140
caa gtc aac gtt ttc gat tct gga ata gca atc ggt gtc tcc gtc tct 483			
Gln Val Asn Val Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser			
145	150	155	
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His Lys Leu Ile Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp			
160	165	170	
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175	180	185	
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 Tyr Val Asp Gln Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala  
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aca agg aga ttt gta ttt ggt gtg aaa gcc ata tct tca att caa gat 723  
 Thr Arg Arg Phe Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp  
 225 230 235

gaa gcg aag agc gag tcc gtg ccc aag cca tca cga gtt cat gcc gtc 771  
 Glu Ala Lys Ser Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val  
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 Thr Gly Phe Leu Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr  
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 Ser Gly Thr Thr Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn  
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 305 310 315

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 Gly Ser Val Lys Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly  
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aaa gag gga tat gga aga atg tgc gag tat cta gat ttt cag agg act 1107  
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gaa gaa gag aaa atg gct atg cta gaa caa gat ccc cat ttt cta gcg 1347  
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 430 435 440

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ctcgtgcaat gtttcgattt tgcagtgaat aaggtttaa ttagttcacc agccaatcaa 1461

taaaatgcaa gtatgataga cttgtctac gtatgttacc cgaatgtgtt tccatatgct 1521

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caca atg aaa att cac gtt aag gag tca aca att ata cgc cct gct caa 169

Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln

1 5 10 15

gaa aca ccc aag cat cgc cta caa ata tcc gac cta gac atg att gtg 217

Glu Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val

20 25 30

cca tcc aat tac gtt ccc agt gtg tat ttc tat cgg cgg tcc agt gac 265

Pro Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp

35 40 45

tgc acc gat ttt ttt gaa gtt ggt ttg ctg aag aag gct ctg agc gaa 313

Cys Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu

50 55 60

gtt ctt gtg ccg ttt tac ccc gtt gcc gga agg ttg cag aag gat gaa 361

Val Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu

65 70 75

aat cgc aaa att gag att cta tgt aac gga gag gga gtt ttg ttt ctg 409

Asn Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu

80 85 90 95

gag gcc gaa aca agt tgt ggt att gat gat ttc ggt gac ttc tca caa 457

Glu Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln

100 105 110

ggc tcg aaa ctc ctg acg ctt gtt cca act gtt ggt gat aca aag gat 505

Gly Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp

115 120 125

ata tcc tcc cat cca ctc ttg atg gca cag gta act tat ttc aaa tgt 553

Ile Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys

130 135 140

gga ggc gtt tgt gtt gga act aga gtg aat cat aca ctg gta gat gga 601  
 Gly Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly  
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gct tca gcg tac cat atc atc aac tca tgg gcg gag acg acg cgt ggc 649  
 Ala Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly  
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 Val Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val  
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ggg gtt cca act tct ccc aaa ttc cat cac att gaa tat gac ccg cct 745  
 Gly Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro  
 195 200 205

cct tcc atg aac gct cct cct acc caa aat cct gaa atc att tct acc 793  
 Pro Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr  
 210 215 220

gca atc ctt aac cta tca ctt gat caa atc cac acc ctc aaa gag aaa 841  
 Ala Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys  
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tct aag aca gat cat gaa ccc aac gtc aag tat agt agg atg gcg atc 889  
 Ser Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile  
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cta gca gca cat atc tgg cgt agc atg tgt aaa gcg cgc gga tta tct 937  
 Leu Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser  
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gat gat caa gtt agc aag tta cac ttt cct aca gac gga cga cag aga 985  
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 275 280 285

ttg aat cca cca ctc ccg cct gga tat ttt gga aat gta att ttc acc 1033  
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acg tcg ttg acg gct tca tcg ggt gat atc cta agt gaa cca ttg aat 1081  
 Thr Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn  
 305 310 315

cat act gtt gaa aga att caa aaa gca tta aag cgg atg gac gat gag 1129  
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 320 325 330 335

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 Tyr Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn  
 340 345 350

gct cta cgg aaa gga ggc cac att tac aag tgc cct aac ctc aat atc 1225  
 Ala Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile  
 355 360 365

gtc aat ttg gca aat atg cca atg tat gtt gcg aat ttt gga tgg ggc 1273  
 Val Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly  
 370 375 380

cag ccg ata ttt gcg agg atc gtt aac aca tat tat gaa ggg ata gca 1321  
 Gln Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala  
 385 390 395

cat att tat cca agt ccg agc aat gat ggg acc ttg tca gtg gtt ata 1369  
 His Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile  
 400 405 410 415

aac tcg gta gcc gat cac atg cag ctg ttc aag aag ttc ttt tac gag 1417  
 Asn Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu  
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atc ttt gat taaggtaga aagacctagg tattttatat ttctagaaa 1466  
 Ile Phe Asp

tgctactttt tttttttt tttttgggg gcgcaaatgt tgtcttactt ggaattttat 1526

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Arg Gln Lys Val Leu Leu Asp His Leu Arg Pro Ser Ser Ser Ser Asp

10 15 20

gac tct tct ctc tcc gcg tcg gta tgt gcg gct ggg gat agc gct gcg 150

Asp Ser Ser Leu Ser Ala Ser Val Cys Ala Ala Gly Asp Ser Ala Ala

25 30 35

tat gct agg aat cat gtc ttt ggg gac gat gtc gtc atc gtt gca gct 198

Tyr Ala Arg Asn His Val Phe Gly Asp Asp Val Val Ile Val Ala Ala

40 45 50

ttt cgc act cca ctc tgc aag gct aag cgt ggc ggc ttc aag tat act 246

Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg Gly Gly Phe Lys Tyr Thr

55 60 65 70

tat gct gat gat ctc ctc gca cct gtc ctc aag gcc gtg gtt gag aaa 294

Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu Lys Ala Val Val Glu Lys

75 80 85

acc aat ctc aat ccc aag gaa gtc ggg gat att gtt gtc ggt acc gtc 342

Thr Asn Leu Asn Pro Lys Glu Val Gly Asp Ile Val Val Gly Thr Val

90 95 100

ttg gcc cca gga tct cag aga gct agc gaa tgc agg atg gct gct ttc 390

Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu Cys Arg Met Ala Ala Phe

105 110 115

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Tyr Ala Gly Phe Pro Glu Thr Val Pro Val Arg Thr Val Asn Arg Gln

120 125 130

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 135 140 145 150

gca ggg ttt tat gat att ggc att ggt gct ggt ttg gaa tcc atg act 534  
 Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala Gly Leu Glu Ser Met Thr  
 155 160 165

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aat gtt gct cat cgt ttt ggt gtt tca aga cag gag caa gat cag gct 678  
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gca gtt gac tct cat aga aag gca gct gct gct gct gct ggt aga 726  
 Ala Val Asp Ser His Arg Lys Ala Ala Ala Ala Ala Ala Gly Arg  
 215 220 225 230

ttt aaa gat gaa atc atc cct gtg gca acc aag att gtt gat cca aaa 774  
 Phe Lys Asp Glu Ile Ile Pro Val Ala Thr Lys Ile Val Asp Pro Lys  
 235 240 245

tct ggt gat gag aaa cct gtt aca atc tct gtt gat gat ggg att cga 822  
 Ser Gly Asp Glu Lys Pro Val Thr Ile Ser Val Asp Asp Gly Ile Arg  
 250 255 260

aac aca aca ttg gcg gac cta gca aag ctg aag cct gtg ttt aag aaa 870  
 Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu Lys Pro Val Phe Lys Lys  
 265 270 275

gat ggg acc acc act gct ggt aat tct agt caa gtt agt gat ggt gct 918  
 Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser Gln Val Ser Asp Gly Ala  
 280 285 290

gga gct gtt ctc ttg atg aag aga agt gtt gcc gac caa aaa gga ttg 966  
 Gly Ala Val Leu Leu Met Lys Arg Ser Val Ala Asp Gln Lys Gly Leu  
 295 300 305 310

ccg att ctt ggt gta ttc agg aat ttt gtt gct gtt ggt gtg gat cct 1014  
 Pro Ile Leu Gly Val Phe Arg Asn Phe Val Ala Val Gly Val Asp Pro  
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           360              365              370

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 Pro Glu Lys Ile Asn Val Asn Gly Gly Ala Met Ala Ile Gly His Pro  
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aag cgt cgt ggt aaa gac tgc cgc tat gga gtg atc tca atg tgc ata 1302  
 Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly Val Ile Ser Met Cys Ile  
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ggc aca ggg atg ggt gca gcc gct gtt ttt gaa aga gga gac cgg acc 1350  
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 Lys Asp Val Arg  
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gttgggtact accttggtta ttgggatgga atacacatgt agttgggttg ttctcccaga 1570

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Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys

1 5 10

aaa acc gag aac cac gac gtc ggt tgt tta cca aac agc gcc acc tcc 158

Lys Thr Glu Asn His Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser

15 20 25

acc gtt caa aac tca gtc cct tcc acc tcc ctc agc tcc gcc gac gcc 206

Thr Val Gln Asn Ser Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala

30 35 40

acc ctc ggc cgc cac ctg gca cgc cgc ctc gtt caa atc ggc gtc acc 254

Thr Leu Gly Arg His Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr

45 50 55

gac gtc ttc acc gtc ccc ggc gac ttc aac ttg acc ctt ctt gac cac 302

Asp Val Phe Thr Val Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His

60 65 70 75

ctc atc gcc gag ccc ggc ctc acc aac att ggc tgc tgc aac gag ctc 350  
 Leu Ile Ala Glu Pro Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu  
           80              85              90

aac gcc ggg tac gcc gcc gac ggc tac gcg cgg tcg cgt ggc gtc ggc 398  
 Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly  
           95              100             105

gcg tgc gtg gtg act ttc act gtt ggt gga ctg agt gtg ctg aac gcg 446  
 Ala Cys Val Val Thr Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala  
          110             115             120

atc gcc ggc gcg tat agt gag aat ttg ccg gtg att tgt att gtt ggt 494  
 Ile Ala Gly Ala Tyr Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly  
          125             130             135

ggg ccc aac tct aac gat tat ggg act aac cgg att ctt cac cat act 542  
 Gly Pro Asn Ser Asn Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr  
 140              145             150             155

att ggg ttg ccg gac ttc agt caa gag ctc cgg tgc ttt cag acc gtg 590  
 Ile Gly Leu Pro Asp Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val  
          160             165             170

act tgc ttt cag gct gtg gtg aat aat ctg gag gat gca cat gag atg 638  
 Thr Cys Phe Gln Ala Val Val Asn Asn Leu Glu Asp Ala His Glu Met  
          175             180             185

att gat act gca att tcg act gcg ttg aaa gaa agc aag cct gtg tat 686  
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          190             195             200

atc agc att ggc tgc aac ttg gct ggg att cct cat cct act ttc agc 734  
 Ile Ser Ile Gly Cys Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser  
          205             210             215

cgt gaa cct gtt cca ttt tca ttg tct cca aaa ttg agc aat aag tgg 782  
 Arg Glu Pro Val Pro Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp  
 220              225             230             235

gga tta gag gct gca gtg gag gct gct gca gag ttc ttg aac aag gca 830  
 Gly Leu Glu Ala Ala Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala  
          240             245             250

gtg aag cca gtt atg gtg ggc ggg ccc aaa ctg cgc tct gca cat gct 878  
Val Lys Pro Val Met Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala  
255 260 265

ggg gat gcc ttt gtt gaa ctg gct gat gct tct gga ttt gct ctg gct 926  
Gly Asp Ala Phe Val Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala  
270 275 280

gtg atg cca tca gca aag ggg caa gtg cca gag cac cac ccc cat ttc 974  
Val Met Pro Ser Ala Lys Gly Gln Val Pro Glu His His Pro His Phe  
285 290 295

atc gga acg tac tgg ggt gct gtg agc act gcc ttt tgt gct gag att 1022  
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300 305 310 315

gtg gag tct gca gat gca tac ttg ttt gct ggg ccg att ttc aat gac 1070  
Val Glu Ser Ala Asp Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp  
320 325 330

tac agc tca gtt ggg tac tcg ctc ctt ctc aag aaa gag aag gcg atc 1118  
Tyr Ser Ser Val Gly Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile  
335 340 345

att gtg cag cca gat cgt gtg acg ata ggg aat ggc cct aca ttt ggt 1166  
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350 355 360

tgt gtt ctc atg aag gat ttc ctc tta ggc cta gca aag aag ctg aag 1214  
Cys Val Leu Met Lys Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys  
365 370 375

cat aac aac act gct cat gag aac tac cgc agg atc ttt gtg cct gat 1262  
His Asn Asn Thr Ala His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp  
380 385 390 395

ggc cac cct ctg aag gct gca ccc aaa gaa cct ttg agg gtt aat gtt 1310  
Gly His Pro Leu Lys Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val  
400 405 410

ctg ttc aaa cac att cag aat atg ctg tca gct gaa acc gct gtg att 1358  
Leu Phe Lys His Ile Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile  
415 420 425

gct gag aca ggg gac tca tgg ttt aac tgt cag aag ctg aaa ttg cca 1406  
 Ala Glu Thr Gly Asp Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro  
 430 435 440

ccc ggc tgc ggg tat gag ttc caa atg caa tat gga tca att ggt tgg 1454  
 Pro Gly Cys Gly Tyr Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp  
 445 450 455

tca gtt gga gca act ctt ggg tat gct cag gct gta cct gag aag cga 1502  
 Ser Val Gly Ala Thr Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg  
 460 465 470 475

gtg att tct ttc att ggt gat ggg agc ttc cag gtg act gct caa gat 1550  
 Val Ile Ser Phe Ile Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp  
 480 485 490

gtg tcc aca atg att cga aat gga cag aga acc att att ttc ctg ata 1598  
 Val Ser Thr Met Ile Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile  
 495 500 505

aac aat ggt gga tac acc att gaa gtg gaa atc cat gat gga cca tac 1646  
 Asn Asn Gly Gly Tyr Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr  
 510 515 520

aat gtg atc aag aac tgg aac tac act gga ctg gtt gat gca atc cac 1694  
 Asn Val Ile Lys Asn Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His  
 525 530 535

aat ggg gaa ggc aag tgc tgg aca acc aag gtg cgt tgc gaa gag gag 1742  
 Asn Gly Glu Gly Lys Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu  
 540 545 550 555

ctg att gaa gca ata gag act gca aat gga ccc aag aag gat agc ttc 1790  
 Leu Ile Glu Ala Ile Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe  
 560 565 570

tgc ttc att gag gtg att gtt cac aag gat gat acc agc aaa gag ttg 1838  
 Cys Phe Ile Glu Val Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu  
 575 580 585

ctt gag tgg ggg tct agg gtt tct gct gcc aac agc cgc cca cct aat 1886  
 Leu Glu Trp Gly Ser Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn  
 590 595 600

cct cag taaaactctc ctgtgtcata tgaaggcctt cattcacatt cacagattta 1942

Pro Gln

605

gatcaagcca agctcttgtg caaattttcc ttatgtttt cctgtcaact ggagaatggt 2002

gtctgtcaag tttttttac actacagtga tttctggtt gtctgtatat ttccttctga 2062

atattagtat ctcttgattt ttcaattgat caaattctgt gatcctaaat ggtttgtgga 2122

aaaaaaaaa aaaaaaaaaa

2141

<210> 5

<211> 1415

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (56)..(1054)

<223> cDNA

<220>

<223> Strawberry alcohol dehydrogenase

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Met

1

gtg atg tct atc gag cag gaa cac ccc aag aag gca tct gga tgg gct 106

Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp Ala

5

10

15

gca aga gat tca tct ggt gtt ctc tct ccc ttc agt ttc tcc aga agg 154

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg Arg

20

25

30

gaa acc gga gag aaa gac gtg acg ttc aaa gtg atg tac tgt ggg att 202

Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly Ile

35

40

45

tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 250

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr  
50 55 60 65

tat cct ctg gtt cca ggg cat gag att gtt ggt gaa gtg acg gaa gta 298  
Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val  
70 75 80

gga agc aat gta caa aaa ttc aaa gtt gga gac aga gtc ggt gtt gga 346  
Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly  
85 90 95

tgc att gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 394  
Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu  
100 105 110

gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 442  
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr  
115 120 125

gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gat 490  
Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp  
130 135 140 145

gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggt gct 538  
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala  
150 155 160

gcg ccg etc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 586  
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr  
165 170 175

ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc 634  
Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly  
180 185 190

ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag 682  
Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys  
195 200 205

gtt aca gtg att agt aca tcc cct aag aaa gag gag gaa gct cgt aaa 730  
Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg Lys  
210 215 220 225

cac cta gga gct gac tcg ttt ttg gtt agc cgt gac caa gat caa atg 778  
 His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met  
                   230                  235                  240

cag gct gcc att ggt acc atg gat ggg atc att gac acg gtt tct gca 826  
 Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala  
                   245                  250                  255

caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag 874  
 Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys  
                   260                  265                  270

ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctg cca gtt ttt 922  
 Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe  
                   275                  280                  285

cct tta ctc atg gga aga aag atg gta gct ggt agc ggc att ggg ggt 970  
 Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly Gly  
 290                  295                  300                  305

atg aag gag aca caa gag atg ata gat ttt gca gcc aag cac aac att 1018  
 Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn Ile  
                   310                  315                  320

aca gca gac atc gaa gtc ata cca atc gac tac ttg taacctgct 1064  
 Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu  
                   325                  330

atggagcgtc tagtcaaagc agatgtcaga taccgttttg tcatcgacat tggaacaca 1124

ctgaaggcta gctcttaaat tctgcaatcc agactggatc aatgaagaaa caagaacaga 1184

aacggagact gatttagtgt catactcggg gttggttttc ctgtagcat ttttgttgt 1244

ctgctacatg aataatgatc acatgaacaa ctgccttctg tgatgatttg ataataaaag 1304

aatacatgaa caatgatact gccttctttt gtaatgtttt ttactatata atcatttcaa 1364

attattttgc tatatctcta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1415

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<211> 452

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol acyl transferase

<400> 6

Met Glu Lys Ile Glu Val Ser Ile Asn Ser Lys His Thr Ile Lys Pro

1 5 10 15

Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp

20 25 30

Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe Phe Tyr Pro Ile

35 40 45

Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala Asp Leu Arg Gln

50 55 60

Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val

65 70 75 80

Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu

85 90 95

Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys

100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu

115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val

130 135 140

Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile

145 150 155 160

Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe

165 170 175

Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala

180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln

195 200 205

Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala Thr Arg Arg Phe  
210 215 220

Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser  
225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu  
245 250 255

Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr  
260 265 270

Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg  
275 280 285

Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp  
290 295 300

Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser  
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys  
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr  
340 345 350

Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met  
355 360 365

Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe  
370 375 380

Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala  
385 390 395 400

Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr  
405 410 415

Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys  
420 425 430

Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro

435                      440                      445  
 Lys Thr Leu Ile  
 450  
  
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 <223> partial cDNA  
  
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 <223> Strawberry alcohol dehydrogenase  
  
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 Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu  
 1                      5                      10                      15  
  
 gga ggt gtt gga cac atg ggg gtg aag ata gca aag gct atg gga cac 95  
 Gly Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His  
 20                      25                      30  
  
 cat atc acc gtg ata agc tct tct gat aag aag aaa aaa gag gcc ttg 143  
 His Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu  
 35                      40                      45  
  
 gag cat att ggt gct gat gag tac ttg gtg agc tct gat gcc acc caa 191  
 Glu His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln  
 50                      55                      60  
  
 atg caa gag gct atg gac tca ctg gat tac att att gac acc att cca 239  
 Met Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro  
 65                      70                      75  
  
 gtg ttc cac cct ctt gag cct tac ctc tct ttg ttg aag ctt gat ggg 287  
 Val Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly

80	85	90	95
----	----	----	----

aag ttg atc ttg atg ggt gtt atc aac acc cca ttg caa ttt gtc tct 335  
Lys Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser  
100 105 110

cca ttg gtc atg ctt ggg gag gaa gac gat cac cgg gag ctt tgt ggg 383  
Pro Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly  
115 120 125

gag cat gaa gga gat gga gga gat gct cga gtt ctg caa aga gaa aga 431  
Glu His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg  
130 135 140

gct gaa acg atg att gaa gtg gtg aag atg gac tac atc aac gaa gct 479  
Ala Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala  
145 150 155

ttc gaa agg ttg gag aag aac gac gtt agg tac agg ttc gtt gtg gat 527  
Phe Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp  
160 165 170 175

tgt tgc cgg cag caa tct tgatcaataa gaaagaaaga aggcatcatc 575  
Cys Cys Arg Gln Gln Ser  
180

gagtgtgtc ctattttat cgagtactct gtctcatctt atcttaaaca atataaataa 635

acaaagaaaa aaaaaaaaaa aaaaaaaa 663

<210> 8  
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<213> Fragaria x ananassa

<220>  
<221> CDS  
<222> (1)..(528)  
<223> partial cDNA

<220>  
<223> Strawberry alcohol dehydrogenase

<400> 8

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Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu  
1 5 10 15

tgt gaa gac gag ttt aaa aag ata atg aag ata aat ttc atg tct gca 96  
Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala  
20 25 30

tgg ttt ctg gta aat gcc gtt ggc aga aga atg cga gat cat aaa tca 144  
Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser  
35 40 45

gga ggt tcc atc ata ttg ttg acc tcg att gtt gga gct gaa aga ggg 192  
Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly  
50 55 60

ctt tat aca gga gct gtt gcc tat ggt gca tgt tcg gca gca ctg cag 240  
Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln  
65 70 75 80

cag tta gta agg tcg tcg gca ttg gag att gga aaa tac cag atc agg 288  
Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg  
85 90 95

gtt aat gca atc gca cgt ggt ttg cat ttg gaa gat gag ttt cct aag 336  
Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys  
100 105 110

tct gtg gga ata gag aga gca aag aag ctg gtg aat gat gca gtt ccg 384  
Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro  
115 120 125

ctg gag aga tgg ctt gat gtt aaa aat gat gtg gct tca agt gtc ata 432  
Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile  
130 135 140

tat ttg gtc agt gat ggt tca agg tac atg acg ggc aca act ata ttt 480  
Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe  
145 150 155 160

gtt gat ggg gca cag tct ctc gtg agg cct cga atg cgt tct tat atg 528  
Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met

165 170 175

tgattcttgc tcctattata tcctcctage cattattage tacttaggtt tgttcatact 588

tcataggtga actcattage tattcttaca ttgttcctt atgaataaag aagtcaagat 648

tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 694

<210> 9

<211> 1586

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (78)..(1268)

<223> cDNA

<220>

<223> Strawberry aminotransferase

<400> 9

aaaccgtcgg cgtctgtaaa tgcgtcgccg ctccggagaa gacagagtac aagactcagg 60

tgaatgcaa tgccaac atg gcc aag ctt caa gcc ggt tat ctt ttt cca 110

Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro

1 5 10

gag att gcg agg agg agg aat gcg cac ttg cag aag cac cct gat gcg 158

Glu Ile Ala Arg Arg Arg Asn Ala His Leu Gln Lys His Pro Asp Ala

15 20 25

aag ata att cca ctt gga att ggt gat act acc gag cca att cca gaa 206

Lys Ile Ile Pro Leu Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu

30 35 40

tat ata acc tct gca atg gca aag aga gca ctt gcc atg tcc acc cta 254

Tyr Ile Thr Ser Ala Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu

45 50 55

gag ggt tac agt ggt tat gga cct gaa caa ggt gaa aag cca ctg aga 302

Glu Gly Tyr Ser Gly Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg

60 65 70 75

gtt gca att gct aaa acg ttt tat ggc gac ctt ggc ata gag gaa gat 350  
Val Ala Ile Ala Lys Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp  
80 85 90

gac ata ttt gtt tct gat ggg gca aaa tgt gac ata tcc cgc ctt cag 398  
Asp Ile Phe Val Ser Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln  
95 100 105

gtt ctt ttt ggg gcg gat aaa aca ata gca gtg caa gat cca tcg tat 446  
Val Leu Phe Gly Ala Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr  
110 115 120

ccg gct tat gta gac tca agt gtt att atg ggc cag aca gga cag tat 494  
Pro Ala Tyr Val Asp Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr  
125 130 135

cag aaa tct gtt cag aag ttt gga aac atc gag tac atg agg tgt act 542  
Gln Lys Ser Val Gln Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr  
140 145 150 155

ccc gat aat gga ttt ttt cct gat ctg tcc tct act aag cga aca gat 590  
Pro Asp Asn Gly Phe Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp  
160 165 170

atc ata ttt ttc tgt tca cca aac aat cct act ggt tct gct gca aca 638  
Ile Ile Phe Phe Cys Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr  
175 180 185

agg gag caa ctg aca caa ctt gta aag ttt gcc aag gat aat ggt tca 686  
Arg Glu Gln Leu Thr Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser  
190 195 200

atc ata gtc tat gat tct gca tat gcc atg tat atg tca gat gat aat 734  
Ile Ile Val Tyr Asp Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn  
205 210 215

cca cgc tcc atc ttt gaa atc cct gga gct aaa gat gtt gca ctt gag 782  
Pro Arg Ser Ile Phe Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu  
220 225 230 235

aca tca tca ttt agt aag tat gcc gga ttc act gga gtt cgt ttg ggg 830  
Thr Ser Ser Phe Ser Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly  
240 245 250

tgg act gtg gtt cca aag cag ttg cag tat tca gat ggt ttt caa gtt 878  
 Trp Thr Val Val Pro Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val  
           255              260              265

gcc aag gat ttc aac cgc att gtt tgt act tgc ttc aat ggt gca tcc 926  
 Ala Lys Asp Phe Asn Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser  
           270              275              280

act att atc caa gct ggt ggt ctg gct tgc ctt caa cca aag ggt gtt 974  
 Thr Ile Ile Gln Ala Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val  
           285              290              295

aag gct atg cac ggt gtg ata aat ttc tac aaa gaa aat act aag atc 1022  
 Lys Ala Met His Gly Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile  
 300              305              310              315

ata atg gag acg ttt aac tct ctt ggc ttt aac gtg tat gga ggg aca 1070  
 Ile Met Glu Thr Phe Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr  
           320              325              330

aac gct cca tat gtg tgg gtc cac ttc cct gga caa agc tcc tgg gat 1118  
 Asn Ala Pro Tyr Val Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp  
           335              340              345

gtg ttt gct gag atc ctt gag aag act cat gtg gta acc aca cct gga 1166  
 Val Phe Ala Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly  
           350              355              360

agt ggc ttt gga cct ggt ggt gaa ggt ttc atc agg gta agt gcc ttt 1214  
 Ser Gly Phe Gly Pro Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe  
           365              370              375

gga cac agg aaa aat ata tta gaa gca tgt aaa aga ttc aag caa tta 1262  
 Gly His Arg Lys Asn Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu  
 380              385              390              395

tac aag tgaggactgc ggatctgaat ttagaccag ttctactgc atgctagtgt 1318  
 Tyr Lys

aacctatttg cctcccattt ccgttctatg ctaaatttt tagcacgttc caattccgta 1378

ttcagtttgt cggctttagt ttatgaatta tggagatttt agctattgta aaaatgattc 1438

gatcagcctt gtttcatgt gttacactta attgttgtaa catttgtgag gatcagaagc 1498

tttgattctg ttgctagaa tagtataatt ttacctaaat aaagtgggtg atctttcttg 1558

gcctgcaaaa aaaaaaaaaa aaaaaaaaaa 1586

<210> 10

<211> 1471

<212> DNA

<213> Cucumis melo

<220>

<221> CDS

<222> (1)..(1368)

<223> cDNA

<220>

<223> Honey dew melon alcohol acyl transferase

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Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala  
1 5 10 15

cca gca aat cct aca ccc tat gaa ttt aaa caa ctt tct gat gtg gat 96  
Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp  
20 25 30

gat caa caa agc tta agg ctt caa ttg cca ttc gta aat atc tat ccc 144  
Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro  
35 40 45

cat aat cca agt ttg gag gga aga gat cca gtg aag gta ata aag gaa 192  
His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu  
50 55 60

gca att gga aag gcg ttg gtg ttc tac tat cct tta gca gga aga ttg 240  
Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu  
65 70 75 80

aga gaa ggg cca ggt aga aag ctt ttt gtt gaa tgt aca ggt gaa gga 288  
Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly  
85 90 95

atc ttg ttt att gaa gcg gat gca gat gtg agc tta gaa gaa ttt tgg 336  
 Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp  
           100              105              110

gat act ctt cca tat tca ctt tca agc atg cag aac aat att ata cat 384  
 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His  
           115              120              125

aac gct tta aat tct gat gaa gtc ctc aat tct cca tta ttg ctc att 432  
 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile  
           130              135              140

cag gtg aca cga ctc aag tgt gga ggt ttc att ttt ggt ctt tgt ttc 480  
 Gln Val Thr Arg Leu Lys Cys Gly Phe Ile Phe Gly Leu Cys Phe  
           145              150              155              160

aat cat act atg gca gat ggt ttt ggt att gtc caa ttc atg aag gct 528  
 Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala  
           165              170              175

aca gcg gag ata gct cgt gga gct ttt gct cca tct att tta cca gta 576  
 Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val  
           180              185              190

tgg caa aga gct ctc tta acc gca aga gac cct ccc aga atc act ttt 624  
 Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe  
           195              200              205

cgc cac tat gaa tac gac caa gta gtc gac atg aag agc ggc ctc att 672  
 Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile  
           210              215              220

cca gtc aat agc aag atc gat caa tta ttc ttc ttt agc caa ctt caa 720  
 Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln  
           225              230              235              240

atc tcc acc ctt cgc caa act ttg cca gcc cac ctt cac gat tgc cct 768  
 Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro  
           245              250              255

tcc ttc gag gtc ctc act gcc tat gtt tgg cgc ctc cgt acc ata gcc 816  
 Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala  
           260              265              270

ctt caa ttt aag cca gag gag gaa gtg cgg ttt ctt tgc gta atg aat 864  
 Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn  
           275              280              285

cta cgc tcg aag atc gac ata cca tta ggg tat tat ggt aat gcg gta 912  
 Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val  
           290              295              300

gtt gtt cct gca gta atc acc acc gct gcg aag ctt tgt ggg aac cca 960  
 Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro  
 305              310              315              320

ctt ggt tat gct gta gac ttg att agg aag gcc aag gct aag gca acg 1008  
 Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr  
           325              330              335

atg gag tac ata aag tct acg gtg gat ctt atg gtg att aaa gga cga 1056  
 Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg  
           340              345              350

ccc tat ttc act gta gtt gga tca ttt atg atg tca gac cta acg aga 1104  
 Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg  
           355              360              365

att ggg gtt gaa aac gtg gac ttt gga tgg gga aag gcc att ttt gga 1152  
 Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly  
           370              375              380

gga cct aca acc aca ggg gcc aga att aca cga ggt ttg gta agc ttt 1200  
 Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe  
 385              390              395              400

tgt gta cct ttc atg aat aga aat gga gaa aag gga act gcg tta agt 1248  
 Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser  
           405              410              415

cta tgc ttg cct cct cca gcc atg gaa aga ttt agg gca aat gtt cat 1296  
 Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His  
           420              425              430

gcc tcg ttg caa gtg aaa caa gtg gtt gat gca gtt gat agc cat atg 1344  
 Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met  
           435              440              445

caa act att caa tct gct tcg aaa taaataatat tgttgaaggt gggctctgagt 1398

Gln Thr Ile Gln Ser Ala Ser Lys

450 455

tgactcgacc atatcgatgc atgcaagctt gatccggctg ctaacaaagc ccgaaaggaa 1458

gctgagttgc tgt 1471

<210> 11

<211> 1485

<212> DNA

<213> Malus sp.

<220>

<221> CDS

<222> (1)..(1362)

<223> cDNA

<220>

<223> Apple alcohol acyl transferase

<221> misc\_feature

<222> (1425)..(1425)

<223> N is any nucleic acid

<400> 11

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Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile

1 5 10 15

act ccg gca aag tca acg cct caa gaa aca aag ttt ctc tca gat att 96

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile

20 25 30

gac gac caa gaa agc ttg aga gtt cag att cca atc ata atg tgt tac 144

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr

35 40 45

aaa gac aac cct tca ctt aat aaa aat cgt aat ccc gtt aag gca att 192

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile

50 55 60

agg gaa gcc tta agt aga gca tta gtg tat tac tac ccc tta gct gga 240

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly  
65                      70                      75                      80

agg ctt agg gaa ggg cct aat aga aag ctc gtg gtc gat tgc aat ggt 288  
Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly  
                    85                      90                      95

gaa ggt atc ttg ttc gtt gag gct tct gct gat gtc aca ctt gag caa 336  
Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln  
                    100                      105                      110

cta gga gac aaa att cta ccc cct tgt cca ctt tta gag gag ttc tta 384  
Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu  
                    115                      120                      125

tat aat ttt cca ggc tct gat gga att att gat tgt cct ttg ctg ctg 432  
Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu  
                    130                      135                      140

att cag gtg acc tgt ctt aca tgt gga ggt ttc ata ctt gca ttg cgc 480  
Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg  
145                      150                      155                      160

cta aac cac aca atg tgt gat gca gct gga ttg ctc ttg ttc ctg acc 528  
Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr  
                    165                      170                      175

gcc atc gcg gag atg gca aga ggc gca cat gca cca tct att cta cca 576  
Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro  
                    180                      185                      190

gtg tgg gag aga gag ctc ttg ttc gct cga gat cca cca aga att aca 624  
Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr  
                    195                      200                      205

tgt gct cgt cat gaa tat gaa gac gtg att ggt cat tct gat ggc tca 672  
Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser  
                    210                      215                      220

tac gca tcc agt aac cag tca aac atg gtt caa cga tct ttc tac ttt 720  
Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe  
225                      230                      235                      240

ggt gcc aag gag atg aga gtc ctt cga aaa cag att cca ccc cac cta 768  
 Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu  
           245              250              255

att tcc act tgc tcc aca ttt gac ttg atc aca gct tgt ttg tgg aaa 816  
 Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys  
           260              265              270

tgt cgc act ctt gca ctt aac att aat cca aaa gag gct gtt cga gtt 864  
 Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val  
           275              280              285

tca tgc att gtc aat gca cga gga aag cac aac aat gta cgt ctt ccc 912  
 Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro  
           290              295              300

ttg gga tac tat ggc aat gca ttt gca ttt cca gct gca att tcg aag 960  
 Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys  
 305              310              315              320

gct gaa cct cta tgc aaa aat cca ctg gga tat gct ttg gag ttg gtg 1008  
 Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val  
           325              330              335

aag aag gct aaa gct acc atg aat gaa gaa tac tta aga tca gtg gca 1056  
 Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala  
           340              345              350

gat ctt ttg gta cta aga ggg cga cct caa tat tca tcg aca gga agt 1104  
 Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser  
           355              360              365

tat tta ata gtt tct gat aat acg cgt gta ggt ttt gga gat gtc aat 1152  
 Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn  
           370              375              380

ttt gga tgg gga cag ccg gta ttt gct gga ccc gtc aag gcc ttg gat 1200  
 Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp  
 385              390              395              400

ttg att agc ttc tac gtt caa cac aaa aac aac aca gag gat gga ata 1248  
 Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile  
           405              410              415

ttg gta cca atg tgt ttg cca tcc tcg gcc atg gag aga ttt cag cag 1296  
 Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln  
           420              425              430

gaa cta gag agg att act cag gaa cct aag gag gat ata tgt aac aac 1344  
 Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn  
           435              440              445

ctt aga tca act agt caa tgatgtaagt gttaaagta atgcactttc 1392  
 Leu Arg Ser Thr Ser Gln  
           450

tgtaatgtag agttgtgtct cttggaactt atcncaagag ttatagctgt tatccaaagg 1452

tctgaatggt attaaaaaat agccaataat aag 1485

<210> 12  
 <211> 1291  
 <212> DNA  
 <213> Musa sp.

<220>  
 <221> CDS  
 <222> (1)..(1257)  
 <223> cDNA

<220>  
 <223> Banana alcohol acyl transferase

<400> 12  
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 Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys  
           1              5              10              15

ggg gtc acg ccg acg ggc tcg ctc ggc ctc tcc gcc atc gac cgg gtg 96  
 Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val  
           20              25              30

ccc ggc ctc agg cat atg gtg cgg tcg cta cac gtg ttc agg caa ggc 144  
 Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly  
           35              40              45

cgg gag ccg gcc agg atc atc agg gaa gca ctg tcg aag gcg ctg gtg 192

Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val  
50 55 60

aag tac tac ccc ttc gcg ggg cgg ttc gtg gac gat ccc gag ggc ggc 240  
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly  
65 70 75 80

ggc gag gtt cgt gtc gct tgc act ggc gag ggc gct tgg ttc gtc gag 288  
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu  
85 90 95

gcc aag gcg gac tgc agc ttg gag gac gtg aag tac ctc gat ctc ccg 336  
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro  
100 105 110

ctc atg atc cct gag gac gcg ctc ctg ccc aag ccc tgc ccg gga ctg 384  
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu  
115 120 125

aac ccc ctc gac ctc cct ctc atg ctg cag gtg aca gag ttc gtg ggc 432  
Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly  
130 135 140

ggc gga ttc gtg gtc ggc ctc atc tcc gtc cat acc atc gcc gac ggc 480  
Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly  
145 150 155 160

ctc ggc gtc gtc cag ttc atc aac gcc gtc gcc gag atc gcc cgt ggc 528  
Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly  
165 170 175

ctg ccg aag ccc acc gtg gag cct gca tgg tcc cgg gag gtc ata ccc 576  
Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro  
180 185 190

aac cca cct aag ctg cct ccc ggt ggc ccg ccc gtg ttc ccc tcc ttc 624  
Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe  
195 200 205

aag ctg ctc cac gcc acc gtc gac cta tcc cct gac cac atc gat cac 672  
Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His  
210 215 220

gtc aag tcc cga cac ttg gag ctc acc ggc cag cgc tgc tct acc ttc 720  
Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe  
225 230 235 240

gac gtc gcc atc gcc aac ctg tgg cag tcc cgc acg cgc gcc atc aac 768  
Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn  
245 250 255

ctg gac cca ggc gtc gac gtg cac gtg tgc ttc ttc gcc aac act cgc 816  
Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg  
260 265 270

cac ctg ttg cgc cag gtc gtc ctc ctg ccc ccc gag gat ggc tac tac 864  
His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr  
275 280 285

ggc aac tgc ttc tac ccg gtg acc gcc acc gcc cca agc ggc agg atc 912  
Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile  
290 295 300

gca tcg gcc gag ctc atc gat gtc gtc agc atc atc agg gac gcc aag 960  
Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys  
305 310 315 320

tcg agg ctg ccg ggc gag ttc gcc aag tgg gct gcc ggg gat ttc aag 1008  
Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys  
325 330 335

gac gac cct tac gag ctc agc ttc acg tac aac tcg ctg ttc gtg tcg 1056  
Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser  
340 345 350

gac tgg acc cgg ctc ggc ttc ctc gac gtc gac tac ggc tgg ggc aag 1104  
Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys  
355 360 365

ccc ctc cac gtt ata ccg ttc gcg tac ttg gac atc atg gcg gtc ggc 1152  
Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly  
370 375 380

atc atc ggg gcg ccg ccg gcg ccg caa aag ggg act cgg gtg atg gcg 1200  
Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala  
385 390 395 400

cag tgc gtc gag aag gag cac atg cag gcg ttc ctg gaa gag atg aaa 1248  
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys  
                   405                  410                  415

ggc ttc gct taaaccagca gcagtgtagt acttgcagt atcc 1291  
 Gly Phe Ala

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 <211> 1488  
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 <213> Fragaria vesca

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 atg gag aaa att gag gtc agt ata att tcc aaa cac acc atc aaa cca 48  
 Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro  
           1                  5                  10                  15

tca act tcc tct tca cca ctt cag cct tac aag ctt acc ctg ctc gac 96  
 Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp  
                   20                  25                  30

cag ctc act cct cca tcg tat gtc ccc atg gta ttc ttc tac ccc att 144  
 Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile  
           35                  40                  45

act ggc cct gca gtc ttc aat ctt caa acc cta gct gac tta aga cat 192  
 Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His  
           50                  55                  60

gcc ctt tcc gag act ctc act ttg tac tat cca ctc tct gga agg gtc 240  
 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val  
           65                  70                  75                  80

aaa aac aac cta tac atc gat gat ttt gaa gag ggt gtc cca tac ctt 288  
 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu

85	90	95	
gag gct cga gtg aac tgt gac atg aat gat ttt cta agg ctt ccg aaa 336			
Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys			
100	105	110	
atc gag tgc cta aat gag ttt gtt cca ata aaa cca ttt agt atg gaa 384			
Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu			
115	120	125	
gca ata tct gat gag cgt tac cct ttg ctc gga gtt caa gtt aac att 432			
Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile			
130	135	140	
ttc aac tcc gga ata gca atc ggg gtc tcc gtc tct cac aag ctc atc 480			
Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile			
145	150	155	160
gat gga aga act tca gac tgt ttt ctc aag teg tgg tgt gct gtt ttt 528			
Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe			
165	170	175	
cgt ggt tct cgt gac aaa atc ata cat cct aat ctc tct caa gca gca 576			
Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala			
180	185	190	
ttg ctt ttc cca cca aga gat gac ttg cct gaa aag tat gcc cgt cag 624			
Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln			
195	200	205	
atg gaa ggg tta tgg ttt gtc gga aaa aaa gtt gct aca agg aga ttt 672			
Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe			
210	215	220	
gta ttt ggt gcg aaa gcc ata tct gta att caa gat gaa gca aag agc 720			
Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser			
225	230	235	240
gag tcc gtg ccc aag cca tca cga gtt cag gct gtc act agt ttt ctc 768			
Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu			
245	250	255	
tgg aaa cat cta atc gct act tct cgg gca cta aca tca ggt act act 816			

Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr  
260 265 270

tca aca aga ctt tct ata gca acc cag gta gtg aac ata aga tca cgg 864  
Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg  
275 280 285

agg aac atg gag aca gtg tgg gat aat gcc att gga aac ttg ata tgg 912  
Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp  
290 295 300

ttc gct ccg gcc ata cta gag cta agt cat aca aca cta gag atc agt 960  
Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser  
305 310 315 320

gat ctt aag ctg tgt gac ttg gtt aac ttg ctc aat gga tct gtc aaa 1008  
Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys  
325 330 335

caa tgt aac ggt gat tac ttt gag act ttc atg ggt aaa gag gga tat 1056  
Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr  
340 345 350

gga agc atg tgc gag tat cta gat ttt cag agg act atg agt tct atg 1104  
Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met  
355 360 365

gaa cca gca cca gag att tat tta ttc acg agc tgg act aat ttt ttc 1152  
Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe  
370 375 380

aac caa ctt gat ttt gga tgg ggg agg aca tca tgg att gga gtt gca 1200  
Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala  
385 390 395 400

gga aaa att gaa tct gca ttt tgc aat ctc aca aca tta gtt cca aca 1248  
Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr  
405 410 415

cca tgc gat act gga att gaa gcg tgg gtg aat cta gaa gaa gaa aaa 1296  
Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys  
420 425 430

atg gct atg cta gaa caa gat ccc cag ttt cta gca cta gca tct cca 1344  
 Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro  
 435 440 445

aag acg cta att tca aga tat tgattaagga agattatgcg gctcgtgcaa 1395  
 Lys Thr Leu Ile Ser Arg Tyr  
 450 455

tgtttccatt ttgttgtgat taaggcttaa attagttcac cagccaatca ataagatgca 1455

agtatgatag actcgggtcta cgtatgttat ccg 1488

<210> 14  
 <211> 434  
 <212> PRT  
 <213> Citrus limon  
 <223> Citrus limon alcohol acyl transferase

<400> 14  
 Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln Glu  
 1 5 10 15

Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val Pro  
 20 25 30

Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp Cys  
 35 40 45

Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu Val  
 50 55 60

Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu Asn  
 65 70 75 80

Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu Glu  
 85 90 95

Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln Gly  
 100 105 110

Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp Ile  
 115 120 125

Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys Gly  
130 135 140

Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly Ala  
145 150 155 160

Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly Val  
165 170 175

Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val Gly  
180 185 190

Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro Pro  
195 200 205

Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr Ala  
210 215 220

Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys Ser  
225 230 235 240

Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile Leu  
245 250 255

Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser Asp  
260 265 270

Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg Leu  
275 280 285

Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Thr  
290 295 300

Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn His  
305 310 315 320

Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu Tyr  
325 330 335

Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn Ala  
340 345 350

Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile Val

355                      360                      365  
 Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly Gln  
 370                      375                      380  
 Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala His  
 385                      390                      395                      400  
 Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile Asn  
 405                      410                      415  
 Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu Ile  
 420                      425                      430

Phe Asp

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<220>  
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 Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu  
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acg ccg agg ata tct ctg tgg aac tcc aac gcc gat ctg gtg gtt ccc 96  
 Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro  
 20                      25                      30

cga ttt cat act ccc agc gtt tac ttc tac cgg ccc acc ggg gcc ata 144  
 Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile  
 35                      40                      45

aac ttc ttt gat ggt aag ttg ctc aag gag gct ctc ggc aag gct ctg 192

Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu  
50 55 60

gtg ccg ttc tac cca atg gcg ggg cgg tta aag cgt gac gaa gat gga 240  
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly  
65 70 75 80

agg att gag atc gat tgt aat gct gaa ggc gtc ttg ttt gtt gag gcc 288  
Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala  
85 90 95

gaa act ccc tct gtt att gat gat ttt ggt gac ttt gcg ccc act tta 336  
Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu  
100 105 110

gag ctc aag cag ctc att ccg aca gtg gat tac tcc ggc ggg atc tct 384  
Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser  
115 120 125

acg tat ccc cta ttg gcg tta cag gtt act cac ttc aaa tgt ggt gga 432  
Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly  
130 135 140

gtt tca ctt ggt gta ggt atg caa cac cat gcg gca gat gga ttt tct 480  
Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser  
145 150 155 160

ggt ctt cac ttt gta aac aca tgg tca gac att gct cgt ggt ctt gat 528  
Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp  
165 170 175

gtt aac atc acc ctg ttc att gac cgg act ctg ctc aga gca cag gat 576  
Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp  
180 185 190

ccc cct cag cct act ttc cca cac aca tgg aat acc agg ccg cct cct 624  
Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro  
195 200 205

tcc ctg aaa act cct cca cca gca gtt tct gag cct act gct gtc tcc 672  
Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser  
210 215 220

att ttt aag ttg acg cgg gac cag ctc aac atc ctc aaa gcc aag gcc 720  
 Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala  
 225 230 235 240

aaa gaa gat ggt aac act atc aac tat agc tca tat gag atg ctg gcg 768  
 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala  
 245 250 255

ggt cat gtc tgg aga tct gca tgc aag gca cgc ggc tta tct gat gat 816  
 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp  
 260 265 270

caa gag act aaa ttg tac ata gca act gac gga cgt gct aga tta atc 864  
 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile  
 275 280 285

ccc cca ctt cca cct ggt tac ttt ggg aat gtg ata ttt aca gcc aca 912  
 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr  
 290 295 300

cca atg gca gta gca ggt gat ctc cag tca aag cct ata tgg tat gct 960  
 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala  
 305 310 315 320

gct ggc cag att cat gat gcc ttg gtt cga atg gac aac gac tat tta 1008  
 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu  
 325 330 335

agg tca gcc ctc gat tac cta gag ctt cag cct gat tta tca gca tta 1056  
 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu  
 340 345 350

gtt cgt ggt gcc cat aca ttt agg tgt cca aat ctc ggg att act agt 1104  
 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser  
 355 360 365

tgg gtt aga ctg cca ata cat gat gca gat ttt ggt tgg ggt cca ccc 1152  
 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro  
 370 375 380

aca ttt atg ggg cct ggt ggg att gca tat gaa ggc tta tca ttt gta 1200  
 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val  
 385 390 395 400

ttg cca agc cct aca aat gat ggg agc tta tca gtt gcc atc tct cta 1248  
 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu  
                   405                  410                  415

caa tct gaa cac atg aaa ctg ttt cag aag ttc ttt tat gat att taa 1296  
 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile  
                   420                  425                  430

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                                   Met Asp Leu Gln Ile Thr Cys  
                                   1                  5

acc gaa atc atc aag cct tct teg ccg acg cct caa cac caa agt acc 102  
 Thr Glu Ile Ile Lys Pro Ser Ser Pro Thr Pro Gln His Gln Ser Thr  
                   10                  15                  20

tat aaa ctt tca att att gat caa tta act cct aat gtt tac ttt tcc 150  
 Tyr Lys Leu Ser Ile Ile Asp Gln Leu Thr Pro Asn Val Tyr Phe Ser  
                   25                  30                  35

atc att ctc ttg tat tca aaa gct ggt gaa agt acc gcc aaa act tca 198  
 Ile Ile Leu Leu Tyr Ser Lys Ala Gly Glu Ser Thr Ala Lys Thr Ser  
                   40                  45                  50                  55

gat cac ctc aaa gaa tct ctt tca aat aca tta acc cac tac tat cct 246  
 Asp His Leu Lys Glu Ser Leu Ser Asn Thr Leu Thr His Tyr Tyr Pro  
                   60                  65                  70

tta gct ggg caa ctc aaa tat gat caa ctt att gtt gat tgt aac gac 294

Leu Ala Gly Gln Leu Lys Tyr Asp Gln Leu Ile Val Asp Cys Asn Asp  
75 80 85

caa ggt gtc ccg ttc atc gaa gca cac gtc acc aac gac atg cgt cag 342  
Gln Gly Val Pro Phe Ile Glu Ala His Val Thr Asn Asp Met Arg Gln  
90 95 100

ctt ctt aaa ata cca aat att gat gtt ctc gaa caa ctc cta cca ttc 390  
Leu Leu Lys Ile Pro Asn Ile Asp Val Leu Glu Gln Leu Leu Pro Phe  
105 110 115

aaa ccg cat gag ggt ttt gat tct gat cgt tcc aac cta acc gtt cag 438  
Lys Pro His Glu Gly Phe Asp Ser Asp Arg Ser Asn Leu Thr Val Gln  
120 125 130 135

gtc aat tac ttt ggt tgt gaa gga atg gcg att ggt ctg tgc ttc aga 486  
Val Asn Tyr Phe Gly Cys Glu Gly Met Ala Ile Gly Leu Cys Phe Arg  
140 145 150

cac aaa gtt att gat gca aca acg gct gca ttc ttt gtt aag aac tgg 534  
His Lys Val Ile Asp Ala Thr Thr Ala Ala Phe Phe Val Lys Asn Trp  
155 160 165

ggt gta att gct cgt ggt gct gga gaa att aag gac gtg atc att gat 582  
Gly Val Ile Ala Arg Gly Ala Gly Glu Ile Lys Asp Val Ile Ile Asp  
170 175 180

cat gct tcc ctg ttt ccc gca aga gat tta tcg tgc tta aca aag agt 630  
His Ala Ser Leu Phe Pro Ala Arg Asp Leu Ser Cys Leu Thr Lys Ser  
185 190 195

ggt gac gaa gag ttt ttg aag cca gag tct gaa aca aag cgc ttt gtg 678  
Val Asp Glu Glu Phe Leu Lys Pro Glu Ser Glu Thr Lys Arg Phe Val  
200 205 210 215

ttt gat ggt gcc act ata gct tct tta caa gaa acg ttt gca agt ttt 726  
Phe Asp Gly Ala Thr Ile Ala Ser Leu Gln Glu Thr Phe Ala Ser Phe  
220 225 230

gaa cga cgt cca aca cgc ttt gag gtt gtg tca gca gtt att ttg ggt 774  
Glu Arg Arg Pro Thr Arg Phe Glu Val Val Ser Ala Val Ile Leu Gly  
235 240 245

gct ttg ata act gca acg aga gaa tct gat gat gag tct aac gtt cct 822  
 Ala Leu Ile Thr Ala Thr Arg Glu Ser Asp Asp Glu Ser Asn Val Pro  
           250                  255                  260

gaa cgt ttg gac acg ata att tca gtg aat cta cgg cag aga atg aat 870  
 Glu Arg Leu Asp Thr Ile Ile Ser Val Asn Leu Arg Gln Arg Met Asn  
           265                  270                  275

cca cca ttc ccg gag cat tgc atg ggg aat ata ata tcc ggg gga tta 918  
 Pro Pro Phe Pro Glu His Cys Met Gly Asn Ile Ile Ser Gly Gly Leu  
 280                  285                  290                  295

gtg tat tgg cca ctg gag aaa aaa gtt gat tac ggg tgt tta gca aaa 966  
 Val Tyr Trp Pro Leu Glu Lys Lys Val Asp Tyr Gly Cys Leu Ala Lys  
           300                  305                  310

gag att cat gaa tca ata aag aaa gtg gac gat caa ttt gcg agg aag 1014  
 Glu Ile His Glu Ser Ile Lys Lys Val Asp Asp Gln Phe Ala Arg Lys  
           315                  320                  325

ttc tat ggg gac gca gag ttc ttg aac ctg ccg agg ctt gcg ggt gct 1062  
 Phe Tyr Gly Asp Ala Glu Phe Leu Asn Leu Pro Arg Leu Ala Gly Ala  
           330                  335                  340

gag gat gtg aag aag cgg gag ttt tgg gtt act agt tgg tgc aaa act 1110  
 Glu Asp Val Lys Lys Arg Glu Phe Trp Val Thr Ser Trp Cys Lys Thr  
           345                  350                  355

ccg ctg tat gaa gct gat ttc ggg tgg ggg aat cct aag tgg gca ggc 1158  
 Pro Leu Tyr Glu Ala Asp Phe Gly Trp Gly Asn Pro Lys Trp Ala Gly  
 360                  365                  370                  375

aac tcc atg agg ctt aat cag att act gtt ttc ttt gac agt agt gat 1206  
 Asn Ser Met Arg Leu Asn Gln Ile Thr Val Phe Phe Asp Ser Ser Asp  
           380                  385                  390

ggt gag gga gtt gaa gct tgg gtg ggg ttg ccc aga aaa gac atg gct 1254  
 Gly Glu Gly Val Glu Ala Trp Val Gly Leu Pro Arg Lys Asp Met Ala  
           395                  400                  405

cga ttt gaa aaa gat tct ggc atc ctt gct tac act tcc cct aat cca 1302  
 Arg Phe Glu Lys Asp Ser Gly Ile Leu Ala Tyr Thr Ser Pro Asn Pro  
           410                  415                  420

agc ata ttt tgagggttta ttatttttt attgcactgt ttgttattg 1351  
 Ser Ile Phe  
 425

tactggccttg ctgggaacat attctggcaa atttcgctga tgcaagtatc attctccata 1411

aaaatgtcaa aaaaaaaaaa aaaaa 1436

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<220>  
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 Met Ala  
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gca att gaa aac aga gta aca cta aag aag cat gag gtt acc aaa gtc 105  
 Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr Lys Val  
 5 10 15

acc cct ttc gtc aac ccc aac tca aag acg acg tcg ttt act ctc gat 153  
 Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr Leu Asp  
 20 25 30

ctc acc tat ttc gac ttt ttc tgg ttc aag aat cct cct gtg gaa cgc 201  
 Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val Glu Arg  
 35 40 45 50

ctc ttc ttc tat gag atg act gac ttg acg tgg gat tta ttc aac tcg 249  
 Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe Asn Ser  
 55 60 65

gag atc ctc cca aag ctg aag cac tcc ctt tcc ttc act ctc ctt cat 297  
 Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu Leu His  
           70              75              80

tac ctc cct ctt gct ggt cac atc atg tgg ccg ctg gat gcc gca aag 345  
 Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala Ala Lys  
           85              90              95

cct gcc gtc tac tac ttt ccc gac caa aac gac ggc gtt tca ttc gca 393  
 Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser Phe Ala  
           100             105             110

gtt gct gag tgg tct tcc gag tgc cac gca ggc ttc cat cac ctc tcc 441  
 Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His Leu Ser  
           115             120             125             130

ggc aac gga atc cgc caa gca gtt gaa ttt cat cct ctt gtg ccc cag 489  
 Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val Pro Gln  
           135             140             145

ttg tcg ctt acg gac gat aaa gct gag gta att gcc atc caa ata aca 537  
 Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln Ile Thr  
           150             155             160

ctg ttt ccg aat caa ggc ttc tca att ggt gtt tca tct cac cat gca 585  
 Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His His Ala  
           165             170             175

att ctt gat gga aaa act tcg acc ttg ttc ctg aaa tct tgg gct tat 633  
 Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp Ala Tyr  
           180             185             190

ttg tgc aaa caa tta caa tta tgc cat cac cct tgt ttg tca cct gaa 681  
 Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser Pro Glu  
           195             200             205             210

cta acc cct ctt ctc gac cgg act gtc atc aaa gat ccg aca ggt cag 729  
 Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr Gly Gln  
           215             220             225

gac atg ctg caa ctg aat aag tgg gtt gtc ggg tcg gat aat tcg gat 777  
 Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn Ser Asp  
           230             235             240

ccc cag aag ata cgg agc ttg aag gtt tta cca ttc tta gac tct gag 825  
 Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp Ser Glu  
           245              250              255

tct ctg aac aaa ttg gtc cga gcc aca ttt gag ttg acg cgt gaa gat 873  
 Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg Glu Asp  
           260              265              270

att acg aaa ctc agg cac aag gtt aat cat cag tta tca aaa tca tca 921  
 Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys Ser Ser  
 275              280              285              290

aaa tca aag caa gtt cgt tta tca act ttt gtg ctt aca tta gct tat 969  
 Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu Ala Tyr  
           295              300              305

gtg ttt gtt tgc atg gct aaa gct aaa tta gcc aaa gcc aaa act gaa 1017  
 Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys Thr Glu  
           310              315              320

gct gaa gct gca gca ggt aat gat gaa att aaa aat att att gtg gga 1065  
 Ala Glu Ala Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile Val Gly  
           325              330              335

ttc act gcg gat tat agg agc cgt ttg gat cct cca att cca ctt aat 1113  
 Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro Leu Asn  
           340              345              350

tat ttt ggt aac tgc aat ggg aga cat tgt gag act gca aaa gca agt 1161  
 Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys Ala Ser  
 355              360              365              370

gat ttc gtt caa gaa aat ggg gtt gct ttt gtt gca gag atg tta agt 1209  
 Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met Leu Ser  
           375              380              385

gat atg gtc aaa ggg atc gat gcg gat gcc att gaa gcc aat gat gat 1257  
 Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn Asp Asp  
           390              395              400

aag gtt tca gaa ata ttg gaa att ctg aaa gaa gga gca atg att ttt 1305  
 Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met Ile Phe  
           405              410              415

tct gtg gct ggc tcg acc caa ttt gat gtt tac ggg tcg gat ttc ggg 1353  
 Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp Phe Gly  
 420 425 430

tgg ggg agg ccc aag aag gtg gag att gtg tca ata gat agg aca caa 1401  
 Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg Thr Gln  
 435 440 445 450

gcc atc tct ttg gca gag aga aga gat gga gga ggc ggc gtt gag gtt 1449  
 Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Gly Val Glu Val  
 455 460 465

gga gtt gtt tta gag aag caa caa atg gag gtt ttt gaa tct gta ttt 1497  
 Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser Val Phe  
 470 475 480

gct gat gga ctg aaa aat gat ctt gtt taattaatga tgtatcatct 1544  
 Ala Asp Gly Leu Lys Asn Asp Leu Val  
 485 490

aaatttctca atatattatt ggatcatattc aaaagaaata aattattgcg gattttgtg 1604

accaccaaatt aaaatactct ttttgaaaa aaaaaaaaaa aaaa 1648

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cct tct gag cca acc cca tct acg gtt ttg tct ctc tca gct ctt gat 96

Pro Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp  
20 25 30

tct cag ctt ttc ttg cgt ttc act att gag tat ctc ttg gtc tat aga 144  
Ser Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg  
35 40 45

cct cgc cct ggt ttg gac cca ctt gct acc gtg gct cgt gtc aag tcc 192  
Pro Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser  
50 55 60

gca ctc gcc aaa gcc ttg gtt cct tac tat ccc ctc gcg ggt cgg gtc 240  
Ala Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val  
65 70 75

aga gct aaa caa gac ggg tcg ggc tta ttg gaa gtc gtg tgt cta ggc 288  
Arg Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly  
80 85 90 95

caa ggc gct gtg ttc atc gaa gcc gtc gac cgt gaa agt acg atc acc 336  
Gln Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr  
100 105 110

gat ttt gag agt gct ccc agg tat gtt act cag tgg agg aaa ctg ctg 384  
Asp Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu  
115 120 125

tcg tta tac gtg gcg gat gtt ctc aaa ggg gcc cca cct ctt gtc gtt 432  
Ser Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val  
130 135 140

cag ctg act tgg ctt aga gat gga gcc gca gcg ctc ggt att ggc ttt 480  
Gln Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe  
145 150 155

aac cat tgt gtt tgc gat ggt atc ggc agc gcc gag ttc ctc aac ttg 528  
Asn His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu  
160 165 170 175

ttt act gag tta tgt acg agc cgt cat aac gaa ctg ggt ggt ggc cat 576  
Phe Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His  
180 185 190

tct ctg ccg aaa ccc gtt tgg gat cgc cac cta atg aac tcc tcc tca 624  
 Ser Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser  
           195                  200                  205

tca cgt caa cag cat gca gat aca cgt gcc agc tca gtg agt cac ctg 672  
 Ser Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu  
           210                  215                  220

gaa ttc aac aga gtg gct gat ctt tgt ggt ttt gtt tct cgt ttt tcc 720  
 Glu Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser  
           225                  230                  235

aac gaa agg ctt gtt ccc act tca ata acg ttc gat aaa cga cgc tta 768  
 Asn Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu  
           240                  245                  250                  255

aac gag ctg cgg aag ctg gct ctg tcc acg agt cga ccc agt gag ctg 816  
 Asn Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu  
           260                  265                  270

gct tac acg tca ttt gaa gtt ctt tca gct cat gtg tgg aga agc tgg 864  
 Ala Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp  
           275                  280                  285

gct agg tcg ttg aat ctt ccg tcg aat caa atc ttg aag ctt cta ttt 912  
 Ala Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe  
           290                  295                  300

agc atc aat gta cgt aac cgt gtc aag ccg agt ctc ccc agt ggc tat 960  
 Ser Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr  
           305                  310                  315

tat ggc gat gca ttt gta tta ggc tgt gct caa acg agg gtt aaa gat 1008  
 Tyr Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp  
           320                  325                  330                  335

ttg aca gag aag gac tta ggg cat gca gca atg ttg gtt aaa aag gcg 1056  
 Leu Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala  
           340                  345                  350

aaa gag aga gtt gat agt gag tat gtg aag tcg gtc atc gac tca gtg 1104  
 Lys Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val  
           355                  360                  365

agt cac acg aga gcg tgt ccc gac tca gtc ggg gtg ttg ata gtg tcg 1152  
 Ser His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser  
 370 375 380

cag tgg tca agg cta ggg tta gag aga gtt gac ttt ggg atg ggg agg 1200  
 Gln Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg  
 385 390 395

ccg act caa gtg ggt ccc att tgc tgc gac agg tat tgc ctg ttt cta 1248  
 Pro Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu  
 400 405 410 415

ccg gtt ttc aat cag acg gac gct gtt aag gtg atg gtg gcg gtc ccc 1296  
 Pro Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro  
 420 425 430

aca agt gca gtt gac aag tat gag cat ctc gcg aag ggc tta tgc tgg 1344  
 Thr Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp  
 435 440 445

tgaggaccac accgcatgat gacccaccca tgtaatacgt tgacttataa actcagtttg 1404

acttttaact ttttaacaa gtgatggaat ttcagtgatt gactcatcac ttgatcctg 1464

atccaataaa taattgaatt gagttcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1520

<210> 19

<211> 455

<212> PRT

<213> *Fragaria vesca*

<223> Strawberry vesca alcohol acyl transferase

<400> 19

Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro  
 1 5 10 15

Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp  
 20 25 30

Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile  
 35 40 45

Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His

50                      55                      60  
 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val  
 65                      70                      75                      80  
 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu  
                     85                      90                      95  
 Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys  
                     100                      105                      110  
 Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu  
                     115                      120                      125  
 Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile  
                     130                      135                      140  
 Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile  
 145                      150                      155                      160  
 Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe  
                     165                      170                      175  
 Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala  
                     180                      185                      190  
 Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln  
                     195                      200                      205  
 Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe  
                     210                      215                      220  
 Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser  
 225                      230                      235                      240  
 Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu  
                     245                      250                      255  
 Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr  
                     260                      265                      270  
 Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg  
                     275                      280                      285

Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp  
290 295 300

Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser  
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys  
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr  
340 345 350

Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met  
355 360 365

Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe  
370 375 380

Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala  
385 390 395 400

Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr  
405 410 415

Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys  
420 425 430

Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro  
435 440 445

Lys Thr Leu Ile Ser Arg Tyr  
450 455

<210> 20

<211> 419

<212> PRT

<213> Musa sp.

<223> Banana alcohol acyl transferase

<400> 20

Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys  
1 5 10 15

Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val  
20 25 30

Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly  
35 40 45

Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val  
50 55 60

Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly  
65 70 75 80

Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu  
85 90 95

Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro  
100 105 110

Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu  
115 120 125

Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly  
130 135 140

Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly  
145 150 155 160

Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly  
165 170 175

Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro  
180 185 190

Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe  
195 200 205

Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His  
210 215 220

Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe  
225 230 235 240

Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn

245                      250                      255  
 Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg  
 260                      265                      270  
 His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr  
 275                      280                      285  
 Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile  
 290                      295                      300  
 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys  
 305                      310                      315                      320  
 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys  
 325                      330                      335  
 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser  
 340                      345                      350  
 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys  
 355                      360                      365  
 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly  
 370                      375                      380  
 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala  
 385                      390                      395                      400  
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys  
 405                      410                      415

Gly Phe Ala

<210> 21

<211> 454

<212> PRT

<213> Malus sp.

<223> Apple alcohol acyl transferase

<400> 21

Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile  
 1                      5                      10                      15

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile  
20 25 30

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr  
35 40 45

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile  
50 55 60

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly  
65 70 75 80

Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly  
85 90 95

Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln  
100 105 110

Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu  
115 120 125

Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu  
130 135 140

Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg  
145 150 155 160

Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr  
165 170 175

Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro  
180 185 190

Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr  
195 200 205

Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser  
210 215 220

Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe  
225 230 235 240

Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu

245	250	255
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys		
260	265	270
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val		
275	280	285
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro		
290	295	300
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys		
305	310	315 320
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val		
325	330	335
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala		
340	345	350
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser		
355	360	365
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn		
370	375	380
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp		
385	390	395 400
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile		
405	410	415
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln		
420	425	430
Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn		
435	440	445
Leu Arg Ser Thr Ser Gln		
450		

<210> 22

<211> 431

<212> PRT

<213> *Mangifera indica*

<223> Mango alcohol acyl transferase

<400> 22

Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu

1 5 10 15

Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro

20 25 30

Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile

35 40 45

Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu

50 55 60

Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly

65 70 75 80

Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala

85 90 95

Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu

100 105 110

Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser

115 120 125

Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly

130 135 140

Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser

145 150 155 160

Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp

165 170 175

Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp

180 185 190

Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro

195 200 205

Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser  
210 215 220

Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala  
225 230 235 240

Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala  
245 250 255

Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp  
260 265 270

Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile  
275 280 285

Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr  
290 295 300

Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala  
305 310 315 320

Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu  
325 330 335

Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu  
340 345 350

Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser  
355 360 365

Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro  
370 375 380

Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val  
385 390 395 400

Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu  
405 410 415

Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile  
420 425 430

<210> 23

<211> 426  
 <212> PRT  
 <213> Citrus limon  
 <223> Lemon acyl transferase

<400> 23

Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro  
 1 5 10 15

Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu  
 20 25 30

Thr Pro Asn Val Tyr Phe Ser Ile Ile Leu Leu Tyr Ser Lys Ala Gly  
 35 40 45

Glu Ser Thr Ala Lys Thr Ser Asp His Leu Lys Glu Ser Leu Ser Asn  
 50 55 60

Thr Leu Thr His Tyr Tyr Pro Leu Ala Gly Gln Leu Lys Tyr Asp Gln  
 65 70 75 80

Leu Ile Val Asp Cys Asn Asp Gln Gly Val Pro Phe Ile Glu Ala His  
 85 90 95

Val Thr Asn Asp Met Arg Gln Leu Leu Lys Ile Pro Asn Ile Asp Val  
 100 105 110

Leu Glu Gln Leu Leu Pro Phe Lys Pro His Glu Gly Phe Asp Ser Asp  
 115 120 125

Arg Ser Asn Leu Thr Val Gln Val Asn Tyr Phe Gly Cys Glu Gly Met  
 130 135 140

Ala Ile Gly Leu Cys Phe Arg His Lys Val Ile Asp Ala Thr Thr Ala  
 145 150 155 160

Ala Phe Phe Val Lys Asn Trp Gly Val Ile Ala Arg Gly Ala Gly Glu  
 165 170 175

Ile Lys Asp Val Ile Ile Asp His Ala Ser Leu Phe Pro Ala Arg Asp  
 180 185 190

Leu Ser Cys Leu Thr Lys Ser Val Asp Glu Glu Phe Leu Lys Pro Glu

195	200	205
Ser Glu Thr Lys Arg Phe Val Phe Asp Gly Ala Thr Ile Ala Ser Leu		
210	215	220
Gln Glu Thr Phe Ala Ser Phe Glu Arg Arg Pro Thr Arg Phe Glu Val		
225	230	235 240
Val Ser Ala Val Ile Leu Gly Ala Leu Ile Thr Ala Thr Arg Glu Ser		
245	250	255
Asp Asp Glu Ser Asn Val Pro Glu Arg Leu Asp Thr Ile Ile Ser Val		
260	265	270
Asn Leu Arg Gln Arg Met Asn Pro Pro Phe Pro Glu His Cys Met Gly		
275	280	285
Asn Ile Ile Ser Gly Gly Leu Val Tyr Trp Pro Leu Glu Lys Lys Val		
290	295	300
Asp Tyr Gly Cys Leu Ala Lys Glu Ile His Glu Ser Ile Lys Lys Val		
305	310	315 320
Asp Asp Gln Phe Ala Arg Lys Phe Tyr Gly Asp Ala Glu Phe Leu Asn		
325	330	335
Leu Pro Arg Leu Ala Gly Ala Glu Asp Val Lys Lys Arg Glu Phe Trp		
340	345	350
Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp		
355	360	365
Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr		
370	375	380
Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly		
385	390	395 400
Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu		
405	410	415
Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe		
420	425	

<210> 24  
 <211> 491  
 <212> PRT  
 <213> Citrus limon  
 <223> Lemon acyl transferase

<400> 24  
 Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr  
 1 5 10 15  
 Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr  
 20 25 30  
 Leu Asp Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val  
 35 40 45  
 Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe  
 50 55 60  
 Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu  
 65 70 75 80  
 Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala  
 85 90 95  
 Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser  
 100 105 110  
 Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His  
 115 120 125  
 Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val  
 130 135 140  
 Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln  
 145 150 155 160  
 Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His  
 165 170 175  
 His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp  
 180 185 190

Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser  
195 200 205

Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr  
210 215 220

Gly Gln Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn  
225 230 235 240

Ser Asp Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp  
245 250 255

Ser Glu Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg  
260 265 270

Glu Asp Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys  
275 280 285

Ser Ser Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu  
290 295 300

Ala Tyr Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys  
305 310 315 320

Thr Glu Ala Glu Ala Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile  
325 330 335

Val Gly Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro  
340 345 350

Leu Asn Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys  
355 360 365

Ala Ser Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met  
370 375 380

Leu Ser Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn  
385 390 395 400

Asp Asp Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met  
405 410 415

Ile Phe Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp

420                      425                      430  
 Phe Gly Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg  
 435                      440                      445  
 Thr Gln Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Gly Val  
 450                      455                      460  
 Glu Val Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser  
 465                      470                      475                      480  
 Val Phe Ala Asp Gly Leu Lys Asn Asp Leu Val  
 485                      490

<210> 25  
 <211> 447  
 <212> PRT  
 <213> Citrus limon  
 <223> Lemon acyl transferase

<400> 25  
 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro  
 1                      5                      10                      15  
 Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp Ser  
 20                      25                      30  
 Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg Pro  
 35                      40                      45  
 Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser Ala  
 50                      55                      60  
 Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val Arg  
 65                      70                      75                      80  
 Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly Gln  
 85                      90                      95  
 Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr Asp  
 100                      105                      110  
 Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu Ser

115	120	125	
Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val Gln			
130	135	140	
Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn			
145	150	155	160
His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe			
165	170	175	
Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His Ser			
180	185	190	
Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser Ser			
195	200	205	
Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu			
210	215	220	
Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser Asn			
225	230	235	240
Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn			
245	250	255	
Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu Ala			
260	265	270	
Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala			
275	280	285	
Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe Ser			
290	295	300	
Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr			
305	310	315	320
Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu			
325	330	335	
Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys			
340	345	350	

Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser  
355 360 365

His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln  
370 375 380

Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro  
385 390 395 400

Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro  
405 410 415

Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr  
420 425 430

Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp  
435 440 445

<210> 26

<211> 456

<212> PRT

<213> Cucumis melo

<223> Honey dew melon alcohol acyl transferase

<400> 26

Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala  
1 5 10 15

Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp  
20 25 30

Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro  
35 40 45

His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu  
50 55 60

Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu  
65 70 75 80

Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly  
85 90 95

Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp  
100 105 110

Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His  
115 120 125

Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile  
130 135 140

Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe  
145 150 155 160

Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala  
165 170 175

Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val  
180 185 190

Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe  
195 200 205

Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile  
210 215 220

Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln  
225 230 235 240

Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro  
245 250 255

Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala  
260 265 270

Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn  
275 280 285

Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val  
290 295 300

Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro  
305 310 315 320

Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr

325                      330                      335  
 Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg  
 340                      345                      350  
 Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg  
 355                      360                      365  
 Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly  
 370                      375                      380  
 Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe  
 385                      390                      395                      400  
 Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser  
 405                      410                      415  
 Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His  
 420                      425                      430  
 Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met  
 435                      440                      445  
 Gln Thr Ile Gln Ser Ala Ser Lys  
 450                      455

<210> 27

<211> 397

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry aminotransferase

<400> 27

Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro Glu Ile Ala Arg Arg  
 1                      5                      10                      15

Arg Asn Ala His Leu Gln Lys His Pro Asp Ala Lys Ile Ile Pro Leu  
 20                      25                      30

Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala  
 35                      40                      45

Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly

50	55	60			
Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys					
65	70	75	80		
Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser					
	85	90	95		
Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala					
100	105	110			
Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp					
115	120	125			
Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln					
130	135	140			
Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe					
145	150	155	160		
Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys					
165	170	175			
Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr					
180	185	190			
Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp					
195	200	205			
Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe					
210	215	220			
Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser					
225	230	235	240		
Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro					
245	250	255			
Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn					
260	265	270			
Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala					
275	280	285			

Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly  
290 295 300

Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe  
305 310 315 320

Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val  
325 330 335

Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile  
340 345 350

Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro  
355 360 365

Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn  
370 375 380

Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys  
385 390 395

<210> 28

<211> 458

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry thiolase

<400> 28

Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg  
1 5 10 15

Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala  
20 25 30

Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp  
35 40 45

Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg  
50 55 60

Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu  
65 70 75 80

Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp  
85 90 95

Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu  
100 105 110

Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val  
115 120 125

Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp  
130 135 140

Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala  
145 150 155 160

Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val  
165 170 175

Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro  
180 185 190

Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg  
195 200 205

Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala  
210 215 220

Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr  
225 230 235 240

Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser  
245 250 255

Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu  
260 265 270

Lys Pro Val Phe Lys Lys Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser  
275 280 285

Gln Val Ser Asp Gly Ala Gly Ala Val Leu Leu Met Lys Arg Ser Val  
290 295 300

Ala Asp Gln Lys Gly Leu Pro Ile Leu Gly Val Phe Arg Asn Phe Val

305            310            315            320  
 Ala Val Gly Val Asp Pro Ala Ile Met Gly Val Gly Pro Ala Ala Ala  
           325            330            335  
 Ile Pro Val Ala Val Lys Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp  
           340            345            350  
 Leu Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg  
           355            360            365  
 Asn Lys Leu Gly Leu Asp Pro Glu Lys Ile Asn Val Asn Gly Gly Ala  
           370            375            380  
 Met Ala Ile Gly His Pro Leu Gly Ala Thr Gly Ala Arg Cys Val Ala  
 385            390            395            400  
 Thr Leu Leu His Glu Met Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly  
           405            410            415  
 Val Ile Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala Ala Val Phe  
           420            425            430  
 Glu Arg Gly Asp Arg Thr Asp Glu Leu Cys Asn Ala Arg Lys Val Glu  
           435            440            445  
 Ser Leu Asn Phe Leu Ser Lys Asp Val Arg  
           450            455  
 <210> 29  
 <211> 605  
 <212> PRT  
 <213> Fragaria x ananassa  
 <223> Strawberry pyruvate decarboxylase  
 <400> 29  
 Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His  
   1            5            10            15  
 Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser  
           20            25            30  
 Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His

35	40	45
Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val		
50	55	60
Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro		
65	70	75
		80
Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala		
85	90	95
Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr		
100	105	110
Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr		
115	120	125
Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn		
130	135	140
Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp		
145	150	155
		160
Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala		
165	170	175
Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile		
180	185	190
Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys		
195	200	205
Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro		
210	215	220
Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala		
225	230	235
		240
Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met		
245	250	255
Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val		
260	265	270

Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala  
275 280 285

Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp  
290 295 300

Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp  
305 310 315 320

Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly  
325 330 335

Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp  
340 345 350

Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys  
355 360 365

Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala  
370 375 380

His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys  
385 390 395 400

Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile  
405 410 415

Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp  
420 425 430

Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr  
435 440 445

Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr  
450 455 460

Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile  
465 470 475 480

Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile  
485 490 495

Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr

500                      505                      510  
 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn  
 515                      520                      525  
 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys  
 530                      535                      540  
 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile  
 545                      550                      555                      560  
 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val  
 565                      570                      575  
 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser  
 580                      585                      590  
 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln  
 595                      600                      605

<210> 30  
 <211> 333  
 <212> PRT  
 <213> Fragaria x ananassa  
 <223> Strawberry alcohol dehydrogenase

<400> 30  
 Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp  
 1                      5                      10                      15  
 Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg  
 20                      25                      30  
 Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly  
 35                      40                      45  
 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser  
 50                      55                      60

Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu  
65                      70                      75                      80

Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val  
                    85                      90                      95

Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His  
                    100                      105                      110

Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr  
                    115                      120                      125

Tyr Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala  
                    130                      135                      140

Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly  
145                      150                      155                      160

Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg  
                    165                      170                      175

Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu  
                    180                      185                      190

Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val  
                    195                      200                      205

Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg  
                    210                      215                      220

Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln  
225                      230                      235                      240

Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser  
                    245                      250                      255

Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly  
                    260                      265                      270

Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val  
                    275                      280                      285

Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly

290                    295                    300  
 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn  
 305                    310                    315                    320  
 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu  
                   325                    330  
  
 <210> 31  
 <211> 326  
 <212> PRT  
 <213> *Fragaria x ananassa*  
 <223> Strawberry alcohol dehydrogenase  
  
 <400> 31  
 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val  
 1                    5                    10                    15  
  
 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr  
                   20                    25                    30  
  
 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val  
                   35                    40                    45  
  
 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp  
                   50                    55                    60  
  
 Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu  
 65                    70                    75                    80  
  
 Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr  
                   85                    90                    95  
  
 Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp  
                   100                    105                    110  
  
 Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala  
                   115                    120                    125  
  
 Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr  
                   130                    135                    140  
  
 Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg

145            150            155            160  
 Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser  
           165            170            175  
 Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr  
           180            185            190  
 Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp  
           195            200            205  
 Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val  
           210            215            220  
 Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn  
 225            230            235            240  
 Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro  
           245            250            255  
 Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile  
           260            265            270  
 Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His  
           275            280            285  
 Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr  
           290            295            300  
 Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile  
 305            310            315            320  
 Asp Val Glu Asn Thr Leu  
           325  
  
 <210> 32  
 <211> 278  
 <212> PRT  
 <213> Fragaria x ananassa  
 <223> Strawberry alcohol dehydrogenase  
  
 <400> 32  
 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu

1	5	10	15
Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn			
20	25	30	
Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly			
35	40	45	
Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala			
50	55	60	
Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro			
65	70	75	80
Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly			
85	90	95	
Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu			
100	105	110	
Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr			
115	120	125	
Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu			
130	135	140	
Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala			
145	150	155	160
Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His			
165	170	175	
Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val			
180	185	190	
Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser Leu			
195	200	205	
Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys			
210	215	220	
Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala			
225	230	235	240

Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg  
245 250 255

Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn  
260 265 270

Thr Leu Lys Pro Ala Ile  
275

<210> 33

<211> 283

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 33

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg  
1 5 10 15

Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile  
20 25 30

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr  
35 40 45

Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val  
50 55 60

Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly  
65 70 75 80

Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu  
85 90 95

Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr  
100 105 110

Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp  
115 120 125

Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala  
130 135 140

Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr  
145                    150                    155                    160

Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly  
                  165                    170                    175

Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys  
                  180                    185                    190

Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys  
                  195                    200                    205

His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met  
                  210                    215                    220

Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala  
225                    230                    235                    240

Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys  
                  245                    250                    255

Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe  
                  260                    265                    270

Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp  
                  275                    280

<210> 34

<211> 188

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 34

Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val  
1                    5                    10                    15

Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala  
                  20                    25                    30

Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp  
                  35                    40                    45

Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp  
50 55 60

Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp  
65 70 75 80

Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys  
85 90 95

Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu  
100 105 110

Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser  
115 120 125

Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala  
130 135 140

Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu  
145 150 155 160

Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe  
165 170 175

Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr  
180 185

<210> 35

<211> 1227

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(979)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 35

g gaa aca gga gca acg gac gta aga ttc aaa gtg ttg tac tgt gga gta 49

Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val

1	5	10	15
tgc cat tcg gac ata cac atg gcc aaa aat gat tgg ggg act tct acc 97			
Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr			
20	25	30	
tat cct att gta cct ggg cat gaa ctt gtt ggt gta gta aca gaa gta 145			
Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val			
35	40	45	
gga tgc aaa gta aag aaa ttc aaa agt tgg aga caa ggt cgg tgt tgg 193			
Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp			
50	55	60	
ttg cat ggt cga ctc aga cca act tgc gaa aat tgt atc cat cac cta 241			
Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu			
65	70	75	80
gaa aat tac tgt ccg aat ctg ata caa acc tac ggt tct aaa tac tac 289			
Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr			
85	90	95	
gac gga acc atg aca tac gga ggt tac tcg aac aac atg gtg act gat 337			
Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp			
100	105	110	
gag cac ttc att gtt cgg atc ccg gac aac tta cct ctt gat ggc gct 385			
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala			
115	120	125	
gct ccg ctt cta tgt gcc ggg att aca act tac agc cca tgg aga tat 433			
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr			
130	135	140	
tat gga ctt gac aaa ccc ggt atg cat ctt ggt gtt gaa tgg cct agg 481			
Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg			
145	150	155	160
cgg ttt agg tca cgt ccg ccg tta aat ttg cca ggg ctt tgg ggc tca 529			
Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser			
165	170	175	
agg tta cag tca tta gta cct ccc cta att aaa gaa gga ggc agc tat 577			

Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr  
 180 185 190

gga aca tct ccc gcg ctg atg cat tcc ctg ctt aga act gac caa gat 625  
 Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp  
 195 200 205

cag atg gag gct gcc atg agc aca atg gat ggt atc att gac aca gtt 673  
 Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val  
 210 215 220

cct gca gtt cga cct cta gag cct ttg att tca ttg ttg aag act aat 721  
 Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn  
 225 230 235 240

gga aaa gtt gtt acc gtt ggt ata gca gtg cag cca ctc gat ctc cca 769  
 Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro  
 245 250 255

gtt ttc cct ttg ata ata gga agg aag atg gta gct ggt agt gcc att 817  
 Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile  
 260 265 270

gga ggt atg aaa gag acg caa gag atg att gat ttt gct gct gaa cat 865  
 Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His  
 275 280 285

aac ata aca gct gac atc gag gtc atc ccg att gat tac ctg aac acc 913  
 Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr  
 290 295 300

gca atg gaa cgc gtt gtc aaa aaa gat gtc agg ttt cga ttt gtc atc 961  
 Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile  
 305 310 315 320

gac gtt gag aac aca ttg taagtccgcc taagttttc attcaattct 1009  
 Asp Val Glu Asn Thr Leu  
 325

gttaataaga ctatgcatta atatagact gactctccat aggatggagt tatcagtctt 1069

caaatttcta gacatatttt gtgatcaaat aaatggaatg gctttgtttt cctttccac 1129

taagattaga ttccagttgt attgtttta aagagattga tgttttatt aattgtaaca 1189

gtgttatcag tctaatacatt aaaaaaaaaa aaaaaaaaaa 1227

<210> 36

<211> 1063

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (3)..(836)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 36

gc aaa gtg caa aaa ttt aaa gtt gga gac aaa gtt ggt gtt ggg tgc 47

Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys

1 5 10 15

ttg gta ggc tca tgc aaa act tgc gac agc tgt gct aac gat ttg gag 95

Leu Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu

20 25 30

aac tac tgc ccc aaa cag ata cag act tac ggc gcc aag tac ctt gac 143

Asn Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp

35 40 45

gga aca acc aca tac ggc ggt tac tct gac atc atg gtg gcg gat gag 191

Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu

50 55 60

gcc ttt gta atc cgt att ccg gac aac ctg cct ctt gag ggt gct gct 239

Ala Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala

65 70 75

cct ctc cta tgt gcc gga atc aca act tac agt ccc ctg agg tat ttc 287

Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe

80 85 90 95

gga ctt gac aaa ccc ggc atg cat gtc ggg gtg gtt ggc ctt ggc ggt 335

Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly  
100 105 110

tta ggc cat gtc gcg gtg aag ttt gcc aag gct ttg ggg gtt aat gtc 383  
Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val  
115 120 125

aca gtg atc agt acc tcc gct aat aag aaa gat gaa gct att aaa cac 431  
Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His  
130 135 140

ctt ggt gct gat tct ttc ttg gtc agt cgt gac caa gat cag atg cag 479  
Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln  
145 150 155

gct gcc atg gga aca ttg gac ggt atc atc gac aca gtt tcc gca gtc 527  
Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val  
160 165 170 175

cac ccc ctc cca cct ttg att agt tta ttg aag gct aat gga aag ctt 575  
His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu  
180 185 190

gtt atg gtt gga gca cca gag aag cca ctt gag cta cca gtt ttt tct 623  
Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser  
195 200 205

tta ata atg gga agg aag act tta gcc ggt agt aat atc gga ggt atc 671  
Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile  
210 215 220

aag gag aca caa gag atg ata gat ttg gca gcc aaa cac aac ata acg 719  
Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr  
225 230 235

gcc gac atc gag att atc ccc atc gac tat ttg aac act gct atg gag 767  
Ala Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu  
240 245 250 255

cgt ctt gct aaa ggg gat gtt aga tac cgt ttt gtc atc gac atc gga 815  
Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly  
260 265 270

aac aca ttg aag ccg gcc att taaattgca ttctgatcag aaactgaatc 866

Asn Thr Leu Lys Pro Ala Ile

275

aagcgaggtc gagaggccta cgtaacaatg caaacatgtg ctagcttggt ctggagtag 926

tccttagctt ttctctgatg tattccatct gttttgttca tgtcccatct tattatgaga 986

aaaatgtggg taccgtggat attgaataaa tgaagagcta ctggaacgat ggtttcacaa 1046

aaaaaaaaa aaaaaaa

1063

<210> 37

<211> 1228

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (1)..(849)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 37

gca aga gat tca tct ggt gtc ctc tct ccc ttc aat ttc tcc aga agg 48

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg

1

5

10

15

gaa acc gga gag aaa gac gtt atg ttc aaa gtg ttg tac tgt gga att 96

Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile

20

25

30

tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 144

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr

35

40

45

tat cct ttg gtc ccg ggg cat gag att gtt ggt gaa gtt acg gaa gta 192

Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val

50

55

60

ggg agc aaa gta caa aaa ttt aaa gtt gga gac aga gtc ggt gtt gga 240

Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly  
65 70 75 80

tgc gtt gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 288  
Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu  
85 90 95

gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 336  
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr  
100 105 110

gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gac 384  
Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp  
115 120 125

gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggc gct 432  
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala  
130 135 140

gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 480  
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr  
145 150 155 160

ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc 528  
Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly  
165 170 175

ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag 576  
Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys  
180 185 190

ggt aca gtg atc agt acg tcc cct aag aaa gag gag gaa gct ctt aaa 624  
Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys  
195 200 205

cac cta gga gct gac tcg ttt ttc gtt agc cgt gac caa gat caa atg 672  
His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met  
210 215 220

cag gct gcc att ggt acc atg gat ggg atc att gac aca gtt tct gca 720  
Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala  
225 230 235 240

caa cat cct ctc ctg cct ttg att ggt ttg aag tct cat gga aag 768  
 Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys  
           245              250              255

ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctt cca gtt ttt 816  
 Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe  
           260              265              270

cct tta ctc atg gga aga aag atg ggt agc tgg taaccggcat ttgggggtat 869  
 Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp  
           275              280

gaaggagaca caagagatga tagattttgc tgccaggcac aacataacag cagacatcga 929

agtcatacaa tcgactactt aaacactgct atggagcggt tagtcaaagc agatgtcaga 989

taccgttttg tcatcgacat tggaacaca ctgaaggcta gcacttaaatt tctgcaatcc 1049

agactgtatc aatgaagaaa caagaacaga aactgagatt gatttggtgt catactccgc 1109

ctatggtttt ccttacagca tttttgttg ttgctacat gaataacgat cacatgaact 1169

gtgatgattt gataataaaa gaatacataa acaaaaaaaaa caaaaaaaaa aaaaaaaaa 1228

<210> 38

<211> 852

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (3)..(566)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 38

gt ccc ctg agg tat ttc gga ctt gac aaa ccc ggc atg cat gtc ggg 47  
 Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly  
       1              5              10              15

gtg gtt ggc ctt ggc ggt tta ggc cat gtc gcg gtg aag ttt gcc aag 95

Val Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys  
20 25 30

gct ttg ggg gtt gag gtc aca gtg atc agt acc tcc gct aat aag aaa 143  
Ala Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys  
35 40 45

gat gaa gct att aaa cac ctt ggt gct gat tct ttc ttg gtc agt cgt 191  
Asp Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg  
50 55 60

gac caa gat cag atg cag gct gcc atg gga aca ttg gac ggt atc atc 239  
Asp Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile  
65 70 75

gac aca gtt tct gca gtc cac ccc ctc cca cct ttg att agt tta ttg 287  
Asp Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu  
80 85 90 95

aag gct aat gga aag ctt gtt atg gtt gga gca cca gag aag cca ctt 335  
Lys Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu  
100 105 110

gag cta cca gtt ttt tct tta ata atg gga agg aag act tta gcc ggt 383  
Glu Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly  
115 120 125

agt aat atc gga ggt atc aag gag aca caa gag atg ata gat ttg gca 431  
Ser Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala  
130 135 140

gct aaa cac aac ata acg gcc gac atc gag gtc atc ccc atc gat tat 479  
Ala Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr  
145 150 155

ttg aac act gca atg gag cgt ctt gct aaa ggg gat gtt aga tac cgg 527  
Leu Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg  
160 165 170 175

ttt gtc atc gac atc gga aac aca ttg aag ccg gcc act taaattgca 576  
Phe Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr  
180 185

tttcgatcag aaactgaatc aagcgatgac gagaggccta cgtaacaatg taaacatgtg 636

ctagcttggt cttgtagtag tctttagcat ttctctgatg tactccttct gttttgttca 696

tgttccatct tataataaga ttcttattat gaaaaaaata tggtagcgtg gatattgaat 756

aatgaagaa ctactggaac aatggtttca caaattattt gtggtgctaa aaaaaaaaaa 816

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 852

<210> 39

<211> 181

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 39

Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly

1 5 10 15

Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His

20 25 30

Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu

35 40 45

His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met

50 55 60

Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val

65 70 75 80

Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys

85 90 95

Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro

100 105 110

Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly Glu

115 120 125

His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala

130 135 140

Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe  
 145                    150                    155                    160

Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys  
                   165                    170                    175

Cys Arg Gln Gln Ser  
                   180

<210> 40

<211> 176

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 40

Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu  
   1            5                    10                    15

Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala  
           20                    25                    30

Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser  
       35                    40                    45

Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly  
       50                    55                    60

Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln  
       65                    70                    75                    80

Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg  
           85                    90                    95

Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys  
           100                    105                    110

Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro  
           115                    120                    125

Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile  
       130                    135                    140

Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe  
 145                    150                    155                    160

Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met  
                   165                    170                    175

<210> 41

<211> 283

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 41

Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly  
 1                    5                    10                    15

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys  
                   20                    25                    30

Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu  
                   35                    40                    45

Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His  
                   50                    55                    60

Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe  
 65                    70                    75                    80

Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly  
                   85                    90                    95

Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr  
                   100                    105                    110

Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys  
                   115                    120                    125

Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala  
                   130                    135                    140

Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly  
 145                    150                    155                    160

Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu  
 165 170 175

Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln  
 180 185 190

Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile  
 195 200 205

Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys  
 210 215 220

Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr  
 225 230 235 240

Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val  
 245 250 255

Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu  
 260 265 270

Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp  
 275 280

<210> 42

<211> 1010

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(850)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 42

g gaa act acc atc aat ttt ggg tct aag aag att gca gtt gtt act gga 49

Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly

1 5 10 15

gcc aac aaa ggg att gga ctt gag att agc aag caa tta gct gct aaa 97

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys  
20 25 30

gga gtt ggg gtg gta tta aca gca aga gat gtg aag aga gga aca gaa 145  
Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu  
35 40 45

gct gct gaa aat ctt aag gct tct ggg ttc tct gat gtg gta ttt cat 193  
Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His  
50 55 60

cag cta gat gta aca gag ccg act act att ggt tct ttg gca aac ttt 241  
Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe  
65 70 75 80

ctt gaa acg caa ttt gga aag ctt gac ata ttg gtt aac aat gca gga 289  
Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly  
85 90 95

gtc gtt gga tct gta tac ctc aca gcc gac tat gat cca gtg caa aca 337  
Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr  
100 105 110

tac gag aca gcg agg gat tgt ttg aaa aca aac tat tat ggg ctc aag 385  
Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys  
115 120 125

caa gtc aca gaa gca ctt gtt ccg ctg ctt caa aaa tct gaa gct gca 433  
Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala  
130 135 140

agg ata gtc aat gtc tct tcc gga tta gga cag cta aga aat att gga 481  
Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly  
145 150 155 160

aat gag aag gcc aag aag gag cta gga gat gca gat aac ctc aac gag 529  
Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu  
165 170 175

gag aaa gtg gac aag cta gtt gag gaa ttt ctg gag gat gtg aaa cag 577  
Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln  
180 185 190

gat tcg ata gaa tcc aaa ggc tgg cct cta agt ata tct gcc tac att 625  
 Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile  
 195 200 205

gtc tca aaa gca gct ctg aat gct tat aca aga ctc ttg gca aag aag 673  
 Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys  
 210 215 220

tat ccc cat att gcc ata aac gca gtt ggt cca ggt tat acc aaa aca 721  
 Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr  
 225 230 235 240

gac ctc aat aat aat tcc ggg att ctc aca gtt gaa gaa gct gca gta 769  
 Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val  
 245 250 255

ggt cct gtg agg ctg gct ttg ata gcc gaa act aga att tcc ggc ctc 817  
 Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu  
 260 265 270

ttc ttc aac aga aat gaa gag tcg acc ttt gat taggtcaacg tgatccctga 870  
 Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp  
 275 280

tgaactggac tatttttagat tttcagaatg tgcttgattt tgttgaagta tttatgggat 930

ttgtatgtat actttgatgt atcattgtat taatagagca catgttgtga tcaaaaaaaaa 990

aaaaaaaaa aaaaaaaaaa 1010

<210> 43  
 <211> 243  
 <212> PRT  
 <213> Mangifera indica  
 <223> Mango esterase

<400> 43  
 Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser  
 1 5 10 15

Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg  
 20 25 30

Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp  
35 40 45

Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro  
50 55 60

Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu  
65 70 75 80

Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn  
85 90 95

Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met  
100 105 110

Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys  
115 120 125

Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu  
130 135 140

Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu  
145 150 155 160

Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr  
165 170 175

Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser  
180 185 190

Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu  
195 200 205

Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser  
210 215 220

Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro  
225 230 235 240

Ala Glu Phe

<210> 44

<211> 877

<212> DNA

<213> *Mangifera indica*

<220>

<221> CDS

<222> (1)..(729)

<223> cDNA

<220>

<223> Mango esterase

<400> 44

atg agg cca caa ata gtg tta ttc gga gat tca ata acg gag caa tct 48  
Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser  
1 5 10 15

ttc gga tca ggt ggt tgg ggt tct tct ctt gct gac act tac tct cgc 96  
Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg  
20 25 30

aag gct gat gta tta gtt cgt ggc tat ggt ggc tac aat act aga tgg 144  
Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp  
35 40 45

gca ttg ttc ttg tta tgt cac att ttc cct ctg cac aat aaa ata cct 192  
Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro  
50 55 60

cca gcc gtc acc aca att ttc ttt ggg gct aat gat gca gcc ctt ctt 240  
Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu  
65 70 75 80

ggg aga acg agt gaa agg cag cat gtt ccc gtg gaa gaa tac aag aac 288  
Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn  
85 90 95

aat ctc aga aaa atg gtt cag cat ttg aag gaa gtc tcc ccc acg atg 336  
Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met  
100 105 110

cta gtt gtg ctt att act cca cca cca att gat gag gaa ggg cgt aaa 384  
Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys  
115 120 125

gca tat gca cga tcc gtt tat ggt gag aaa gct atg aaa gag cct gag 432  
 Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu  
           130                  135                  140

agg aca aat gaa atg gct gga gtt tat gct aga cat tgt gtt gaa ctg 480  
 Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu  
           145                  150                  155                  160

gca aaa gat ctt cct gcc att gat ctg tgg tcc aag atg cag gaa aca 528  
 Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr  
                   165                  170                  175

gaa ggt tgg cag aaa aaa ttc ctc agt gat ggg ttg cac ctt aag tca 576  
 Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser  
                   180                  185                  190

gaa ggc aat gca gtg gtt cac caa gaa gtt gtg aga gtt cta aaa gaa 624  
 Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu  
                   195                  200                  205

gca tgg ttt tct cct gaa caa atg cca tat gat ttt cct cac caa tca 672  
 Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser  
           210                  215                  220

gta att gat gga aaa cac cct gag aaa gct ttc caa ctg caa tgc cct 720  
 Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro  
           225                  230                  235                  240

gct gaa ttc tagtcaagac aggcttgga atttgtctc tctttcaatt 769  
 Ala Glu Phe

tttctatttg atgaaaagat ttggactgct ttttctagt catgccaaat gaaacagtgt 829

tagccttttg cctattttat cagatgctga tatgcgctct gtgtcgac 877

<210> 45

<211> 12

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: various fruit

<220>

<223> alcohol acyl transferase motif

<400> 45

Trp Thr Asn Phe Phe Asn Pro Leu Asp Phe Gly Trp

1 5 10

<210> 46

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: various fruit

<220>

<223> alcohol acyl transferase motif

<221> misc\_feature

<222> (1)..(10)

<223> Xaa is any amino acid residue

<400> 46

Leu Xaa Xaa Xaa Tyr Pro Xaa Xaa Gly Arg

1 5 10

<210> 47

<211> 16

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: various fruit

<220>

<223> alcohol acyl transferase motif

<221> misc\_feature

<222> (1)..(16)

<223> Xaa is any amino acid residue

<400> 47

Pro Ser Arg Val Xaa Xaa Val Thr Xaa Phe Leu Xaa Lys Xaa Leu Ile  
 1 5 10 15

<210> 48  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <223> PCR Primer  
 <220>  
 <221> misc\_feature  
 <222>(9)..(9)  
 <223> N is Inosine

<400> 48  
 ggwtgggggnk ctaytcttgc 20

<210> 49  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221>  
 <222>  
 <223> PCR Primer

<220>  
 <223> AAP165

<400> 49  
 cggatccgga gaaaattgag gtcag 25

<210> 50  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221>  
 <222>  
 <223> PCR Primer

<220>

<223> AAP166

<400> 50

cgtcgaccat tgcacgagcc acataatc

28